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OM protein - protein search, using sw model

Run on: October 4, 2004, 12:49:31 ; Search time 324 Seconds
(without alignments)

414.167 Million cell updates/sec

Title: US-09-807-148-2

Perfect score: 2282

Sequence: 1 MLLSVPLLLGLLGLAVAEPA.....EEDKEDEEDVPGQAKDEL 417

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 32179191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2282	100.0	417	10	US-09-807-148-2
2	2282	100.0	417	14	US-10-161-959-29
3	2282	100.0	417	15	US-10-367-093-14
4	2278	99.8	416	15	US-09-828-000-2
5	2278	99.8	416	15	US-10-405-588-2
6	2163.5	94.8	416	14	US-10-316-253-2
7	2163.5	94.8	416	14	US-10-316-253-4
8	2163.5	94.8	416	14	US-10-316-253-6
9	1408.5	61.7	395	15	US-10-369-493-6343
10	1216	53.3	435	12	US-10-425-114-70304
11	1213	53.2	421	15	US-10-767-701-46544
12	1206	52.8	442	12	US-10-425-114-46869
13	1198	52.5	424	16	US-10-437-963-201420
14	1192	52.2	431	16	US-10-767-701-44015
15	1176.5	51.6	420	9	US-09-844-006A-2

ALIGNMENTS

RESULT 1

US-09-906-393A-36
; Sequence 36, Application US/09906393A

; Publication No. US20030039970A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Zhou

; APPLICANT: Xiao, Wuhan

; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED

; FILE REFERENCE: 1720-1-001CIP

; CURRENT APPLICATION NUMBER: US/09/906,393A

; CURRENT FILING DATE: 2001-07-16

; PRIOR APPLICATION NUMBER: 60/218,761

; PRIOR FILING DATE: 2000-07-17

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 36

; LENGTH: 417

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-906-393A-36

Query Match 100.0%; Score 2282; DB 10; Length 417;

Best Local Similarity 100.0%; Pred. No. 7.5e-163;

Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLSVPLLLGLLGLAVAEPAVYFKEQFLDGGTWSWIESKHKSDFGKVLSSGKFGYGE 60
Db 1 MLLSVPLLLGLLGLAVAEPAVYFKEQFLDGGTWSWIESKHKSDFGKVLSSGKFGYGE 60

QY 61 EKDKGLQTSQDARFYALSASPEPPFNKQTLVQVTVKHEQNDCCGGYVKLFNPSLQDT 120
Db 61 EKDKGLQTSQDARFYALSASPEPPFNKQTLVQVTVKHEQNDCCGGYVKLFNPSLQDT 120

QY 121 DMHGDSEYNIIMFGPDICGGPTKKKHVINYKGNVINKDKCKDDETHLYTLVVRDN 180
Db 121 DMHGDSEYNIIMFGPDICGGPTKKKHVINYKGNVINKDKCKDDETHLYTLVVRDN 180

QY 181 TVEVKIDNSQVBSGSLDDWDWFLPPKTKDPASKPEDWDERAKIDDDTDSKPEDWDKPE 240

Sequence 130958, Sequence 114914, Sequence 201427, Sequence 190956, Sequence 46228, A Sequence 5595, A Sequence 46405, A Sequence 69619, A Sequence 48930, A Sequence 114860, Sequence 122222, Sequence 277445, A Sequence 70140, A Sequence 65495, A Sequence 45264, A Sequence 153808, Sequence 46, Appl Sequence 57598, A Sequence 3, Appli Sequence 3, Appli Sequence 44621, A Sequence 54997, A Sequence 38848, A Sequence 129, App Sequence 1095, Ap Sequence 44768, A Sequence 39041, A Sequence 68, Appl Sequence 190356, Sequence 3546, Ap

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Db 181 TYEVKIDNSQVSGSLEDDWDFLPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWPKPE 240
Qy 241 HIPDPAKKPEDWDEMDGWEPPVIONPEYKGEWKPRQIDNPDKYKGTWHPHIDNPEYS 300
Db 241 HIPDPAKKPEDWDEMDGWEPPVIONPEYKGEWKPRQIDNPDKYKGTWHPHIDNPEYS 300
Qy 301 PPSIYAYDNFVGLDLMQVKSFTIDNPLIINDAYAEFGNETGWYTKAAEQMKDK 360
Db 301 PPSIYAYDNFVGLDLMQVKSFTIDNPLIINDAYAEFGNETGWYTKAAEQMKDK 360
Qy 361 QDEEQLKEEEDKKKEEAEADKEDDKDEDEEDKDEDEEDKDEDEEDVFGQAKDEL 417
Db 361 QDEEQLKEEEDKKKEEAEADKEDDKDEDEEDKDEDEEDKDEDEEDVFGQAKDEL 417

RESULT 2
US-10-161-959-29
; Sequence 29, Application US/10161959
; Publication No. US20030096748A1
; GENERAL INFORMATION:
; APPLICANT: Holoshitz, Joseph
; TITLE OF INVENTION: Methods and Compositions for the Treatment of Diseases Associated
; FILE REFERENCE: UN-07135
; CURRENT APPLICATION NUMBER: US/10/161,959
; PRIOR FILING DATE: 2002-10-01
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-161-959-29

Query Match 100.0%; Score 2282; DB 14; Length 417;
Best Local Similarity 100.0%; Pred. No. 7.5e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLSVPLLLGLGLAEPVAVYKQFQFDGQWTSRWIESKHKSDFGKFLVSSGKPYGDE 60
Db 1 MLLSVPLLLGLGLAEPVAVYKQFQFDGQWTSRWIESKHKSDFGKFLVSSGKPYGDE 60
Qy 61 EKDKGLQTSODARFYALSASFEPFSNKGQTLVVQFTVKHEQNDICGGYVVKLFPNSLDQT 120
Db 61 EKDKGLQTSODARFYALSASFEPFSNKGQTLVVQFTVKHEQNDICGGYVVKLFPNSLDQT 120
Qy 121 DMHGDSEYNIMFGPDICGPGTKKVHVFYNYKGVNKLINCKDKDEFFHLYTLIVRPD 180
Db 121 DMHGDSEYNIMFGPDICGPGTKKVHVFYNYKGVNKLINCKDKDEFFHLYTLIVRPD 180
Qy 181 TYEVKIDNSQVSGSLEDDWDFLPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWPKPE 240
Db 181 TYEVKIDNSQVSGSLEDDWDFLPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWPKPE 240
Qy 241 HIPDPAKKPEDWDEMDGWEPPVIONPEYKGEWKPRQIDNPDKYKGTWHPHIDNPEYS 300
Db 241 HIPDPAKKPEDWDEMDGWEPPVIONPEYKGEWKPRQIDNPDKYKGTWHPHIDNPEYS 300
Qy 301 PPSIYAYDNFVGLDLMQVKSFTIDNPLIINDAYAEFGNETGWYTKAAEQMKDK 360
Db 301 PPSIYAYDNFVGLDLMQVKSFTIDNPLIINDAYAEFGNETGWYTKAAEQMKDK 360
Qy 361 QDEEQLKEEEDKKKEEAEADKEDDKDEDEEDKDEDEEDKDEDEEDVFGQAKDEL 417
Db 361 QDEEQLKEEEDKKKEEAEADKEDDKDEDEEDKDEDEEDKDEDEEDVFGQAKDEL 417
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RESULT 3
US-10-367-093-14
; Sequence 14, Application US/10367093
; Publication No. US20030216315A1
; GENERAL INFORMATION:
; APPLICANT: Duke University
; APPLICANT: Nicchitta, Chris
; APPLICANT: Baker-LePain, Julie
; TITLE OF INVENTION: MODULATION OF IMMUNE RESPONSE BY NON-PEPTIDE BINDING STRESS RESPO
; FILE REFERENCE: 160/145
; CURRENT APPLICATION NUMBER: US/10/367,093
; CURRENT FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-093-14

Query Match 100.0%; Score 2282; DB 15; Length 417;
Best Local Similarity 100.0%; Pred. No. 7.5e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLSVPLLLGLGLAEPVAVYKQFQFDGQWTSRWIESKHKSDFGKFLVSSGKPYGDE 60
Db 1 MLLSVPLLLGLGLAEPVAVYKQFQFDGQWTSRWIESKHKSDFGKFLVSSGKPYGDE 60
Qy 61 EKDKGLQTSODARFYALSASFEPFSNKGQTLVVQFTVKHEQNDICGGYVVKLFPNSLDQT 120
Db 61 EKDKGLQTSODARFYALSASFEPFSNKGQTLVVQFTVKHEQNDICGGYVVKLFPNSLDQT 120
Qy 121 DMHGDSEYNIMFGPDICGPGTKKVHVFYNYKGVNKLINCKDKDEFFHLYTLIVRPD 180
Db 121 DMHGDSEYNIMFGPDICGPGTKKVHVFYNYKGVNKLINCKDKDEFFHLYTLIVRPD 180
Qy 181 TYEVKIDNSQVSGSLEDDWDFLPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWPKPE 240
Db 181 TYEVKIDNSQVSGSLEDDWDFLPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWPKPE 240
Qy 241 HIPDPAKKPEDWDEMDGWEPPVIONPEYKGEWKPRQIDNPDKYKGTWHPHIDNPEYS 300
Db 241 HIPDPAKKPEDWDEMDGWEPPVIONPEYKGEWKPRQIDNPDKYKGTWHPHIDNPEYS 300
Qy 301 PPSIYAYDNFVGLDLMQVKSFTIDNPLIINDAYAEFGNETGWYTKAAEQMKDK 360
Db 301 PPSIYAYDNFVGLDLMQVKSFTIDNPLIINDAYAEFGNETGWYTKAAEQMKDK 360
Qy 361 QDEEQLKEEEDKKKEEAEADKEDDKDEDEEDKDEDEEDKDEDEEDVFGQAKDEL 417
Db 361 QDEEQLKEEEDKKKEEAEADKEDDKDEDEEDKDEDEEDKDEDEEDVFGQAKDEL 417

RESULT 4
US-09-828-000-2
; Sequence 2, Application US/09828000
; Publication No. US20030078198A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Calreticulin
US-09-828-000-2

Query Match 99.8%; Score 2278; DB 10; Length 416;
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[illegible]

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; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-4

Query Match          94.8%; Score 2163.5; DB 14; Length 416;
Best Local Similarity 93.8%; Pred. No. 5.7e-154;
Matches 391; Conservative 15; Mismatches 10; Indels 1; Gaps 1;

QY 1 MLLSVPLLLGLGLAFAVPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYGE 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MLLSVPLLLGLGLAFAVPAVYFKEQFLDGDGWTNRWESKHKSDFGKFLVSSGKFGYGE 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 EKDGLQTSQDARFYALSAPFPPSNKQTLVVQFTVTKHEQNDICGGGVKLPFNSLDQT 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 EKDGLQTSQDARFYALSAPFPPSNKQTLVVQFTVTKHEQNDICGGGVKLPFNSLDQT 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 DMHGDSEYNIMFGDPCGPGTKKVHVI FNYKGNVLINKDIRCKDDEFTHLYTLIVRPN 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 DMHGDSEYNIMFGDPCGPGTKKVHVI FNYKGNVLINKDIRCKDDEFTHLYTLIVRPN 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 181 TYEVKIDNSQVESGSLEDDWDFLPPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWDKPE 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 TYEVKIDNSQVESGSLEDDWDFLPPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWDKPE 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 241 HIPDPAKPEDWDEMDGEWEPPIQNPYKGEWKPRQIDNPDKYKGTWHPHIDNPYS 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 HIPDPAKPEDWDEMDGEWEPPIQNPYKGEWKPRQIDNPDKYKGTWHPHIDNPYS 300
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QY 301 PDPSIYAYDNFVGLGLDLQVKSQGTIFDNFLITNDEAYAEFGNETGWVTKAAEKQMDK 360
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 PDANIYAYDSFAVLGLDLQVKSQGTIFDNFLITNDEAYAEFGNETGWVTKAAEKQMDK 360
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 361 QDEORLKEEEDKKRKEEAEADKDEDDKDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 417
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 QDEORLKEEEDKKRKEEAEADKDEDDKDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 416

RESULT 9
US-10-369-493-6343
; Sequence 6343, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6343
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6343

Query Match          61.7%; Score 1408.5; DB 15; Length 395;
Best Local Similarity 63.6%; Pred. No. 2.1e-97;
Matches 250; Conservative 57; Mismatches 81; Indels 5; Gaps 4;

QY 8 LLGLGLAFAVPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYGEEDKGLQ 67
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 LLAIVAVVSAE--VYFKEEFNDA-SWEKRWVSKHDDFGAFKLSAGKEFFVESRDQGIQ 62
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 68 TSQDARFYALSAPF--PFSNKQTLVVQFTVTKHEQNDICGGGVKLPFNSLDQTDHGD 126
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 TSQDARFYRAAKFKDKDFSNKGTLLVIQYTVKHEQIDCGGGYVKVMRADADGLDFHGET 122
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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QY 127 EYNMFGPDICGPGTKKVHVIFNYKGNVLINKDKODFTHLYTLIVRPNTVEVKI 186
Db 123 PYNMFGPDICGP-TRRVHVLNYKGNKLIKEITCKSDHLTHLYTLINSNTVEVKI 181
QY 187 DNSQVSGSLEDWDFLPPKKIKDPDASKPEDWDERAKIDDDPTDSKPEDWDXPEHIPDPD 246
Db 182 DGSQAQTGSLEEDWDLPPAKIKDPDPAKPEDWDEREYIDDAEDAKPEDWEXPEHIPDPD 241
QY 247 AKKPEDWDEMGWEPVPIQNPYKGEWKPRQIDNPYKGTWVIHPEIDNPYSPPSIY 306
Db 242 AKKPEDWDEMGWEPVPIQNPYKGEWKPRQIDNPYKGTWVIHPEIDNPYSPPSIY 301
QY 307 AYDNFVGLDLQVKSGLTFDNLITNDAYAEFGNETGWYTKAAEKQKDKDEROR 366
Db 302 SYESWGAIGFOLQVKSGLTFDNLITNDAYAEFGNETGWYTKAAEKQKDKDEROR 361
QY 367 LKBEEDKKRKEEAEADKEDDDKDERDEDE 399
Db 362 KAEEARKKAEKEAKKDDDEEKEEHEGHD 394

RESULT 10
US-10-425-114-70304
; Sequence 70304, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 70304
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Zea mays subsp. mexicana
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMROTEOSINT102C08_FLI.pep
US-10-425-114-70304

Query Match 53.3%; Score 1216; DB 12; Length 435;
Best Local Similarity 53.8%; Pred. No. 6,3e-83;
Matches 228; Conservative 69; Mismatches 105; Indels 22; Gaps 8;

QY 4 SVPLLLGLGLAUAEPAYVFKQFLDGDGWTSRWIESKHKSD---FGKFLSSGKFYGD 60
Db 24 AVAALLALASVAAGVFFQKEF--EDGWESRWVWSEWKKDENMAGENWHTSGKXNGDA 81
QY 61 EYKGLQTSQARYALASPEPSNKGOTLVQFTVKHEQNDICGGYVKKLFPNSLDQT 120
Db 82 E-DKGIQTSERYFYAISAEYFESFNKDKTLVLQFSVHEQKLDCCGGYVKKLGGVDQK 140
QY 121 DMHGDSEYNMFGPDICGPGTKKVHVIFNYKGNVLINKDKODFTHLYTLIVRPD 180
Db 141 KFGDTSINMFGPDICGPGTKKVHVIFNYKGNVLINKDKODFTHLYTLIVRPD 200
QY 181 TYEVKIDNSQVSGSLEDWDFLPPKKIKDPDASKPEDWDERAKIDDDPTDSKPEDWDX-P 239
Db 201 TYSILIDNEEKQTSIYEHWDILPPKKIKDPDASKPEDWDERAKIDDDPTDSKPEDWDX-P 260
QY 240 EHIPDPDAKPEDWDEMGWEPVPIQNPYKGEWKPRQIDNPYKGTWVIHPEIDNPY 299
Db 261 KEIPDPDAKPEDWDEMGWEPVPIQNPYKGEWKPRQIDNPYKGTWVIHPEIDNPY 320
QY 300 SPDPSIAYDNFVGLDLQVKSGLTFDNLITNDAYAEFGNETGWYTKAAEKQKDK 359
Db 321 KDDPIYAFDSLKYGIELWQVKSGLTFDNLITNDAYAEFGNETGWYTKAAEKQKDK 380
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QY 360 KODEEQRUKKEEEDKKR---KEEBAEDKEDDEDEDEED---BEDKBEDEEDVPGQA 413
Db 381 EAEK---KKEEEDAAKGDDDEDDLEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 431
QY 414 KDEL 417
Db 432 HDEL 435

RESULT 11
US-10-767-701-46544
; Sequence 46544, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 46544
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C5075_1.pep
US-10-767-701-46544

Query Match 53.2%; Score 1213; DB 16; Length 421;
Best Local Similarity 54.0%; Pred. No. 1e-82;
Matches 227; Conservative 69; Mismatches 110; Indels 14; Gaps 7;

QY 4 SVPLLLGLGLAUAEPAYVFKQFLDGDGWTSRWIESKHKSD---FGKFLSSGKFYGD 60
Db 10 AVAALLALASVAAGVFFQKEF--EDGWESRWVWSEWKKDENMAGENWHTSGKXNGDA 67
QY 61 EYKGLQTSQARYALASPEPSNKGOTLVQFTVKHEQNDICGGYVKKLFPNSLDQT 120
Db 68 E-DKGIQTSERYFYAISAEYFESFNKDKTLVLQFSVHEQKLDCCGGYVKKLGGVDQK 126
QY 121 DMHGDSEYNMFGPDICGPGTKKVHVIFNYKGNVLINKDKODFTHLYTLIVRPD 180
Db 127 KFGDTPYSIMFGPDICGPGTKKVHVIFNYKGNVLINKDKODFTHLYTLIVRPD 186
QY 181 TYEVKIDNSQVSGSLEDWDFLPPKKIKDPDASKPEDWDERAKIDDDPTDSKPEDWDX-P 239
Db 187 TYSILIDNEEKQTSIYEHWDILPPKKIKDPDASKPEDWDERAKIDDDPTDSKPEDWDX-P 246
QY 240 EHIPDPDAKPEDWDEMGWEPVPIQNPYKGEWKPRQIDNPYKGTWVIHPEIDNPY 299
Db 247 KEIPDPDAKPEDWDEMGWEPVPIQNPYKGEWKPRQIDNPYKGTWVIHPEIDNPY 306
QY 300 SPDPSIAYDNFVGLDLQVKSGLTFDNLITNDAYAEFGNETGWYTKAAEKQKDK 359
Db 307 KDDPIYAFDSLKYGIELWQVKSGLTFDNLITNDAYAEFGNETGWYTKAAEKQKDK 366
QY 360 KODEEQRUKKEEEDKKR---KKEEBAEDKEDDEDEDEDEDEDEDEDEDEDEDEDEDE 417
Db 367 EAEK---KKEEBAAGKGGDEDDLEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 421

RESULT 12
US-10-425-114-46869
; Sequence 46869, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
```

```
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 46869
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73073A05_FLI.pep
US-10-425-114-46869

Query Match      52.8%; Score 1206; DB 12; Length 442;
Best Local Similarity 53.2%; Pred. No. 3.6e-82;
Matches 223; Conservative 72; Mismatches 112; Indels 12; Gaps 6;

QY  4  SVPLLLGLGLAVAEPAVYFKEQFLDGDGWTSWIESKHSD---FGKFVLSGKFGYDE 60
DB  31  AVAALLALASVAAGVFFQKEF--EDGWSRWKSEWKDENMAGENHTSGKWNDA 88
QY  61  EKDGLQTSODARFYALSASFEPFSNKGQTLVQFTVKHEQNDCCGGYVKLPFNSLDO 119
DB  89  E-DKGIQTSDEYRFYALSAEYFEPFSNKGQTLVQFSVKHEQKLDCCGGYVKLLGGVDQ 147
QY  120  TMHGDSYNIIMFGPDICGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYLIVRPD 179
DB  148  KFGGDTSYIMFGPDICGYSYTKKVHTILTQKGNHLIKDVPCTDQLTHVYTLIIIPD 207
QY  180  NTEVKIDNSQVSGSLEDWDWFLPPKKIKDPAKPEDWDERAKIDDPDTSKPEDWDK- 238
DB  208  ATYSILIDNEKDTGSIYEHWDILPPKKIKDPEAKKPEDWDDKEYIPDPEDKKPREGYDI 267
QY  239  PEHIPDPAKPEDWDEMDGEWEPVIONPYKGEWKPRQIDNPDKYGTWVHHPIDNPE 298
DB  268  KPEIPDPAKPEDWDEEDGEGTAPTIPNPKYKGPWKQKKIKNPYQGWKAPMIDNPD 327
QY  299  YSDPSIYAYDNFVGLDLWLQVKSQTIIPDNFLINDEAYAEFGNETGWVTKAAEKQMK 358
DB  328  FKDDPYIYAFDSLKYIGIELWQVKSQTLIPDNIIITDDPALAKTFAEETWKGHKEAKAF 387
QY  359  DKDEORLKEEEDKKRKEEAEDEKDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 417
DB  388  DEAEK-----KXEEADAAGKGGDEDDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 442

RESULT 13
US-10-437-963-201420
; Sequence 201420, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 201420
; LENGTH: 424
; -TYPE: PRT
; ORGANISM: Oryza sativa

; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 46869
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73073A05_FLI.pep
US-10-425-114-46869

Query Match      52.8%; Score 1206; DB 12; Length 442;
Best Local Similarity 53.2%; Pred. No. 3.6e-82;
Matches 223; Conservative 72; Mismatches 112; Indels 12; Gaps 6;

QY  4  SVPLLLGLGLAVAEPAVYFKEQFLDGDGWTSWIESKHSD---FGKFVLSGKFGYDE 60
DB  31  AVAALLALASVAAGVFFQKEF--EDGWSRWKSEWKDENMAGENHTSGKWNDA 88
QY  61  EKDGLQTSODARFYALSASFEPFSNKGQTLVQFTVKHEQNDCCGGYVKLPFNSLDO 119
DB  89  E-DKGIQTSDEYRFYALSAEYFEPFSNKGQTLVQFSVKHEQKLDCCGGYVKLLGGVDQ 147
QY  120  TMHGDSYNIIMFGPDICGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYLIVRPD 179
DB  148  KFGGDTSYIMFGPDICGYSYTKKVHTILTQKGNHLIKDVPCTDQLTHVYTLIIIPD 207
QY  180  NTEVKIDNSQVSGSLEDWDWFLPPKKIKDPAKPEDWDERAKIDDPDTSKPEDWDK- 238
DB  208  ATYSILIDNEKDTGSIYEHWDILPPKKIKDPEAKKPEDWDDKEYIPDPEDKKPREGYDI 267
QY  239  PEHIPDPAKPEDWDEMDGEWEPVIONPYKGEWKPRQIDNPDKYGTWVHHPIDNPE 298
DB  268  KPEIPDPAKPEDWDEEDGEGTAPTIPNPKYKGPWKQKKIKNPYQGWKAPMIDNPD 327
QY  299  YSDPSIYAYDNFVGLDLWLQVKSQTIIPDNFLINDEAYAEFGNETGWVTKAAEKQMK 358
DB  328  FKDDPYIYAFDSLKYIGIELWQVKSQTLIPDNIIITDDPALAKTFAEETWKGHKEAKAF 387
QY  359  DKDEORLKEEEDKKRKEEAEDEKDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 417
DB  388  DEAEK-----KXEEADAAGKGGDEDDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 442

RESULT 14
US-10-767-701-44015
; Sequence 44015, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 44015
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(431)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C10317_1.pep
US-10-767-701-44015

Query Match      52.2%; Score 1192; DB 16; Length 431;
Best Local Similarity 53.1%; Pred. No. 3.9e-81;
Matches 229; Conservative 62; Mismatches 110; Indels 30; Gaps 8;

QY  3  LSVPLLLGLGLAVAEPAVYFKEQFLDGDGWTSWIESKHSD---FGKFVLSGKFGYD 59
DB  15  VAAALIALASVAGVFFQKEF--DDGWBDRWVKSQWKKDDNTAGWENHTSGKWNKD 72
QY  60  EKDGLQTSODARFYALSASFEPFSNKGQTLVQFTVKHEQNDCCGGYVKLPFNSLDO 119
```

```
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 46869
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73073A05_FLI.pep
US-10-425-114-46869

Query Match      52.5%; Score 1198; DB 16; Length 424;
Best Local Similarity 53.1%; Pred. No. 1.4e-81;
Matches 221; Conservative 69; Mismatches 108; Indels 18; Gaps 5;

QY  4  SVPLLLGLGLAVAEPAVYFKEQFLDGDGWTSWIESKHSD---FGKFVLSGKFGYDE 60
DB  14  AVAALLALASVAAGVFFQKEF--EDGWSRWKSEWKDENMAGENHTSGKWNDA 71
QY  61  EKDGLQTSODARFYALSASFEPFSNKGQTLVQFTVKHEQNDCCGGYVKLPFNSLDO 120
DB  72  E-DKGIQTSDEYRFYALSAEYFEPFSNKGQTLVQFSVKHEQKLDCCGGYVKLLGGVDQ 130
QY  121  DMHGDSYNIIMFGPDICGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYLIVRPD 180
DB  131  KFGGDTSYIMFGPDICGYSYTKKVHTIFTQKGNHLIKDVPCTDQLSHVYTLIIIPDA 190
QY  181  TYEYKIDNSQVSGSLEDWDWFLPPKKIKDPAKPEDWDERAKIDDPDTSKPEDWDK-P 239
DB  191  TYTILIDNVEKQSGSIYEHWDILPPKKIKDPEAKKPEDWDDKEYIPDPEDKKPREGYDIP 250
QY  240  EHIPPDPDAKPEDWDEMDGEWEPVIONPYKGEWKPRQIDNPDKYGTWVHHPIDNPEY 299
DB  251  KEIPDPAKPEDWDEEDGEGTAPTIPNPKYKGPWKQKKIKNPYQGWKAPMIDNPD 310
QY  300  SPSPSIYAYDNFVGLDLWLQVKSQTIIPDNFLINDEAYAEFGNETGWVTKAAEKQMK 359
DB  311  KDPPYIYAFDSLKYIGIELWQVKSQTLIPDNIIITDDPALAKTFAEETWKGHKEAKAF 370
QY  360  KDDEORLKEEEDKKRKEEAEDEKDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 415
DB  371  -----EAEKKKEEAEAKAGDEDDDDLEDEDEDEDEDEDEDEDEDEDEDEDEDE 415

RESULT 14
US-10-767-701-44015
; Sequence 44015, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 44015
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(431)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C10317_1.pep
US-10-767-701-44015

Query Match      52.2%; Score 1192; DB 16; Length 431;
Best Local Similarity 53.1%; Pred. No. 3.9e-81;
Matches 229; Conservative 62; Mismatches 110; Indels 30; Gaps 8;

QY  3  LSVPLLLGLGLAVAEPAVYFKEQFLDGDGWTSWIESKHSD---FGKFVLSGKFGYD 59
DB  15  VAAALIALASVAGVFFQKEF--DDGWBDRWVKSQWKKDDNTAGWENHTSGKWNKD 72
QY  60  EKDGLQTSODARFYALSASFEPFSNKGQTLVQFTVKHEQNDCCGGYVKLPFNSLDO 119
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Db 73 AD-DKGIQTSEDYRFYAIHQYEFNSKDKTLVLQFSVKHEQKLDGCGGYLKLLGSDVDQ 131
Qy 120 TDMGDSSEYNYMFGPDICGPGTKVHVIFNYKGNVLINKDIRCKDDDEFTHLYTLIVRPD 179
Db 132 KKGCGDTPYSIMFGPDICGVTATKKVHAILTNGKGNHLIKKELPGETDQLTHVYTLIIRPD 191
Qy 180 NTVSVKIDNSOVESGLEDWDLPPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWDK- 238
Db 192 ATYSILIDNDEKQSGSYDWDILPPKKIKDPEAKPEDWDDKEYIPDPEDKAPGEGYDDI 251
Qy 239 PEHIPDPDAKPEDWDEMDGEMPEPPVIONPEYKGEWKPRQIDNPDPYKGTWHPIDNPE 298
Db 252 PKEIPDPDAKPEDWDEEDGCEWTAPINPEYKGPWKQKKIKNPDPYKGNKAPLIDNPD 311
Qy 299 YSPDPSIYAVDNFVGLDLWQVKSITFDNFIITNDEAYABEFGNETWGTAAEKQMK 358
Db 312 FKDDFYIYAFDSLXHGIELWQVKSITFDNFIITDPEYAKKLAIVETWGTQKDAEKA 371
Qy 359 DKQDEEQRLEKEEEDKKRKEE-----EEAEKKEDE--DKDEDEDEED-----KEEDEE 406
Db 372 D-----EAEKKRLEECFSLXESASSKODDDLDVDEDEDDADDKADHSDTDEA 420
Qy 407 EDVFGQAKDEL 417
Db 421 EDSEEAKHDEL 431

RESULT 15

US-09-844-006A-2
; Sequence 2, Application US/09844006A
; Patent No. US20020083496A1
; GENERAL INFORMATION:
; APPLICANT: Wyatt, Sarah
; APPLICANT: Tsou, Pei-Lan
; APPLICANT: Robertson, Dominique
; APPLICANT: Boss, Wendy
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH INCREASES IN CALCIUM STORES
; FILE REFERENCE: 5051.503
; CURRENT APPLICATION NUMBER: US/09/844.006A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,233
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Zea mays
US-09-844-006A-2

Query Match 51.6%; Score 1176.5; DB 9; Length 420;
Best Local Similarity 51.9%; Pred. No. 5.5e-80;
Matches 217; Conservative 74; Mismatches 116; Indels 11; Gaps 5;
Qy 4 SVPELLIGLGLAFAEPAYVKEQELDGGGTSRWIESKHKSD---FGKFVLSGKGYGDE 60
Db 10 AVAALLAASVAAGVFFQKEF--EDGWSRWKSEWKDENMAGENWHTSGKMGDA 67
Qy 61 EKDKGLQTSQDARFALSASPEFNSKQTLVQFTVKHEQNIIDCGGYVKLPFNSLDQT 120
Db 68 E-DKGIQTSEDYRFYAIQAEPFNSKDKTLVLQFSVKHEQKLDGCGGYVKLLGGVDQK 126
Qy 121 DMHGDSSEYNYMFGPDICGPGTKVHVIFNYKGNVLINKDIRCKDDDEFTHLYTLIVRPD 180
Db 127 TLGGTSTYSIISRPDISYSTKRVHTILTQDKGNHLIKKQVPCQDQTLTHVYTFIIRPD 186
Qy 181 TYEVKIDNSQVESGLEDWDLPPKKIKDPEAKPEDWDERAKIDDPDTSKPEDWDK-P 239
Db 187 TYSILIDNDEKHTGSIYEHWDILPPKKIKDPEAKPEDWDDKEYIPDPEDKAPGEGYDDIP 246
Qy 240 EHIPDPDAKPEDWDEMDGEMPEPPVIONPEYKGEWKPRQIDNPDPYKGTWHPIDNPEY 299
Db 247 KEIPDPDAKPEDWDEEDGCEWTAPINPEYKGPWKQKKIKNPDPYKGNKAPLIDNPD 305

Qy 300 SPDPISIYAYDNFVGLDLWQVKSITFDNFIITNDEAYABEFGNETWGTAAEKQMKD 359
Db 307 KDDPYIYAFDLSKYIGIELWQVKSITFDNFIITDDPALAKTFAETWGHKHEAKAAFD 366
Qy 360 KQCEPQRLEKEEEDKKRKEEAEADKEDDEDEDEDEDEDEDEDEDEDEDEDEDEDE 417
Db 367 EAEK---KKEEEDAAKGGDDDDLEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 420

Search completed: October 4, 2004, 13:01:15
Job time : 326 secs

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OM protein - protein search, using sw model

Run on: October 4, 2004, 12:49:26 ; Search time 23 Seconds
(without alignments)
936.001 Million cell updates/sec

Title: US-09-807-148-2
Perfect score: 2282
Sequence: 1 MLLSVPELLGLGLAVAEPA.....EDKKEDEEDVPGQAKDEL 417

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2278	99.8	416	4	US-09-828-000-2
2	1224.5	53.7	415	3	US-08-675-816-2
3	971	42.6	180	4	US-09-828-000-3
4	799	35.0	593	1	US-08-296-362-2
5	731.5	32.1	610	4	US-09-976-594-947
6	641.5	28.1	542	3	US-08-675-816-6
7	340	14.9	61	4	US-09-828-000-4
8	327	14.3	61	4	US-09-828-000-8
9	189	8.3	35	4	US-09-828-000-7
10	184.5	8.1	714	2	US-08-990-114-3
11	184.5	8.1	714	4	US-09-241-333-3
12	184.5	8.1	740	1	US-08-257-073-5
13	175.5	7.7	1162	2	US-08-728-323A-2
14	175.5	7.7	1162	4	US-09-298-568-2
15	175.5	7.7	1162	4	US-09-410-399-2
16	163	7.1	905	2	US-08-574-959A-9
17	163	7.1	905	3	US-09-357-014-9
18	163	7.1	1135	2	US-08-574-959A-7
19	163	7.1	1135	3	US-09-357-014-7
20	154	6.7	1312	4	US-09-345-882-29
21	151	6.6	27	4	US-09-828-000-5
22	151	6.6	740	3	US-09-022-983-5
23	150.5	6.6	546	3	US-08-935-855-20
24	149	6.5	411	2	US-08-741-134-6
25	146	6.4	754	3	US-09-214-564A-2
26	146	6.4	764	4	US-09-370-838-67
27	143.5	6.3	197	4	US-09-486-147-40

28	143.5	6.3	240	2	US-08-114-555A-8	Sequence 8, Appli
29	143.5	6.3	240	3	US-08-559-397A-14	Sequence 14, Appli
30	137	6.0	633	1	US-08-458-477A-5	Sequence 5, Appli
31	137	6.0	633	2	US-09-033-153-5	Sequence 5, Appli
32	137	6.0	633	3	US-09-325-430B-5	Sequence 5, Appli
33	137	6.0	765	2	US-08-663-112-2	Sequence 7, Appli
34	137	6.0	1166	4	US-09-200-650E-7	Sequence 26, Appli
35	137	6.0	3052	2	US-08-557-122A-26	Sequence 26, Appli
36	137	6.0	3052	4	US-08-282-666-26	Sequence 5, Appli
37	135	5.9	295	2	US-08-679-765-5	Sequence 5, Appli
38	135	5.9	295	3	US-09-196-525-5	Sequence 5, Appli
39	135	5.9	295	3	US-09-318-317-5	Sequence 22, Appli
40	135	5.9	295	4	US-09-177-165A-22	Sequence 194, App
41	134.5	5.9	231	3	US-09-461-697-194	Sequence 192, App
42	134.5	5.9	232	3	US-09-461-697-192	Sequence 190, App
43	134.5	5.9	238	3	US-09-461-697-190	Sequence 188, App
44	134.5	5.9	257	3	US-09-461-697-188	Sequence 186, App
45	134.5	5.9	272	3	US-09-461-697-186	

ALIGNMENTS

RESULT 1

US-09-828-000-2
; Sequence 2, Application US/09828000
; Patent No. 6596690

GENERAL INFORMATION:
; APPLICANT: Government of the United States of America

; TITLE OF INVENTION: Vasostatin as Marrow Protectant

; FILE REFERENCE: 4239-55414

; CURRENT APPLICATION NUMBER: US/09/828,000

; CURRENT FILING DATE: 2001-04-06

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2

; LENGTH: 416

; TYPE: PRT

; ORGANISM: Calreticulin

US-09-828-000-2

Query Match 99.8%; Score 2278; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 5.6e-199; Indels 0; Gaps 0;
Matches 416; Conservative 0; Mismatches 0;

Qy	1	MLLSVPELLGLGLAVAEPAVYFKQFLDGCWTSRTESKHSDFGKPVLSGGFYGDE	60
Db	1	MLLSVPELLGLGLAVAEPAVYFKQFLDGCWTSRTESKHSDFGKPVLSGGFYGDE	60
Qy	61	EKDKGLOTSQDARFYALSASFEPFNKGOTLVVQFTVXHEQNIIDCGGVYKLPFNSLDDT	120
Db	61	EKDKGLOTSQDARFYALSASFEPFNKGOTLVVQFTVXHEQNIIDCGGVYKLPFNSLDDT	120
Qy	121	DMHGDSEYIMFGPDICGPGTKKHVIFNYKGNVLINKDIRCKDDETHLYTLIVRPN	180
Db	121	DMHGDSEYIMFGPDICGPGTKKHVIFNYKGNVLINKDIRCKDDETHLYTLIVRPN	180
Qy	181	TYEVKIDNSQVSGSLEDWDWFLPPKIKDPASKEPDWDERAKIDDDPTDSKPEDWDKDE	240
Db	181	TYEVKIDNSQVSGSLEDWDWFLPPKIKDPASKEPDWDERAKIDDDPTDSKPEDWDKDE	240
Qy	241	HIPDDPAKPEPDWDERAKIDDDPTDSKPEDWDKDEHPEINPEYS	300
Db	241	HIPDDPAKPEPDWDERAKIDDDPTDSKPEDWDKDEHPEINPEYS	300
Qy	301	PDPSIYAYDNFVGLDLQVKSIGTIFDNFLTNDEAYAEFGNETGWTKAAEQMKDK	360
Db	301	PDPSIYAYDNFVGLDLQVKSIGTIFDNFLTNDEAYAEFGNETGWTKAAEQMKDK	360
Qy	361	QDEEQRLKKEEEDKKKEEAEEDKDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE	416
Db	361	QDEEQRLKKEEEDKKKEEAEEDKDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE	416

RESULT 2
US-08-675-816-2
; Sequence 2, Application US/08675816
; Patent No. 6171864
; GENERAL INFORMATION:
; APPLICANT: Coughlan, Sean J.
; APPLICANT: Winfrey, Jr., Ron J.
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 701 Fifth Ave. Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,816
; FILING DATE: 05-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6171864tenburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 750027.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)-622-4900
; TELEFAX: (206)-682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-675-816-2

Query Match 53.7%; Score 1224.5; DB 3; Length 415;
Best Local Similarity 55.6%; Pred. No. 3.9e-103;
Matches 232; Conservative 57; Mismatches 109; Indels 19; Gaps 8;
QY 8 LIGLLGLAAEPAVYFKEQFLDGGWTSRWIESKHSD---FGKVLSSGKYFGDEEKD 64
DB 11 LLSLLAIAE--VFEEERF--EDGWNRWKSDWKKDENTAGWNYTSGKWNGD-PNDK 65
QY 65 GLQTSQDARFYALSASFEPFSNKGQTLVQVFTVKHEQNDICGGYVVKLPFNSLDQTDWHG 124
DB 66 GIOTSEDFYALSAEFPFSNKGQTLVQVFSVKEQKLDCCGGYMKLLSSSTQKRG 125
QY 125 DSEYINMFGPDICGGTKKHVIFNYKQVNLINKDCKDEFTHLVTLVRPNTYEV 184
DB 126 DTPYSIMFGPDICGVSTKKVHAILNYDNTNHLIKKEVPCETDQLTHVTLVIRPDATYI 185
QY 185 KIDNSQVSGSLEDWDFLPKKIKDPAKPEDWDERAKIDDPDTSKPEDWDK-PEHIP 243
DB 186 LIDNVEKQTSJYTDWLLPPKKIDPEAKPEDWDEKEYFPDEDKKPEGYDIPKEIP 245
QY 244 DPDAKPEDWDEMGWEPVQNPYKGEWKPQIDNPYKGTWHPIDNPYSPDP 303
DB 246 DPDAKPEDWDEEGWETAPTIANPYKGEWKPQIDNPYKGTWHPIDNPYSPDP 305
QY 304 SIYAYDNFVGLDLWQVSGTIFNPLITNDEAAVEFGNETGWTKAAEKQKQDE 363
DB 306 ELYVYVNLKYVGLWQVSGTIFNPLICNDPEYAKQAEETWKNKDAKA---AFEE 362
QY 364 EQLKKEEEDKURKEEBAEDKEDDEDKDEDEEEDKE---EDEEEDVPQAKDEL 417
DB 363 AEKKKEEESKDDPADSDADEDDDDDDTEGEDDGSKSDAEDV---HDEL 415

RESULT 3
US-09-828-000-3
; Sequence 3, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Vasostatin
US-09-828-000-3
Query Match 42.6%; Score 971; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.4e-80;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 EPAYVFEQFLDGGWTSRWIESKHSDRGKFLVSSGKYFGDEEKGLQTSQDARFYAL 77
DB 1 EPAYVFEQFLDGGWTSRWIESKHSDRGKFLVSSGKYFGDEEKGLQTSQDARFYAL 60
QY 78 SASPEPFSNKGQTLVQVFTVKHEQNDICGGYVVKLPFNSLDQTDHGDSEYINMFGPDIC 137
DB 61 SASPEPFSNKGQTLVQVFTVKHEQNDICGGYVVKLPFNSLDQTDHGDSEYINMFGPDIC 120
QY 138 GPQTKKHVIFNYKQVNLINKDCKDEFTHLVTLVRPNTYEVKIDNSQVSGSLE 197
DB 121 GPQTKKHVIFNYKQVNLINKDCKDEFTHLVTLVRPNTYEVKIDNSQVSGSLE 180
RESULT 4
US-08-296-362-2
; Sequence 2, Application US/08296362
; Patent No. 5691306
; GENERAL INFORMATION:
; APPLICANT: Bergeron, John J.M.
; APPLICANT: Thomas, David Y.
; APPLICANT: Wada, Ikuo
; TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF
; TITLE OF INVENTION: PROTEIN TRAFFICKING DISORDERS AND INCREASING SECRETORY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/296,362
; FILING DATE: 25-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deehr, Manya S.
; REGISTRATION NUMBER: 37,120
; REFERENCE/DOCKET NUMBER: 690066.401C1
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-296-362-2

Query Match 35.0%; Score 799; DB 1; Length 593;
Best Local Similarity 34.9%; Pred. No. 3.4e-64;
Matches 182; Conservative 72; Mismatches 133; Indels 134; Gaps 16;

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QY 21 VYKQFLDGDGWTSRWIESKHSD-----FGKFLVSSGKPYGDEEK-----DKGLQTS 69
Db 70 VYFAUSF--DRGLGWLTSKAKKDDTDDEIAK---DGRWEVDKMTKLPDGLKGLVM 124
QY 70 QDARYFALSASF--EPFSNKGQTLVVQFTVKEQNIIDCGGYVKLFPN-----SLDQDTHMG 124
Db 125 SRKAKHA--SAKLNKFLFDTKPLIVQYEVNFQNGIEGGAYVKKLSKTPSLNLDQ--FHD 182
QY 125 DSEYNIMGPDICGPTKVKVHVIENYKGNVLINKDIRCK-----DDEFTHLYTL 174
Db 183 KTYPTIMFGPKDCKGB--DYKLHPIFRHKPKTGVFEKAKRPPDADLKYTFDCKTHLYTL 241
QY 175 IVRPNTYEVKIDNSQVSGSLEDWDFLPP-----KKIKPDASKPEDWDERAKIDDPD 230
Db 242 ILNPDNSPEILLVQSIIVNSGNLNN--DMTPPVNPSREIEDPEDQKPEDWDERPKIPDPA 299
QY 231 SKPEDW-----DKPEHIPPDAKPEDWDEMDGEWEP-----263
Db 300 VKPDDWNEDAPAKIDPEATPDGMLDDEPEYVDPDAEKPEDWDEMDGEWEPAPQIANP 359
QY 264 -----PVIONPEYKGEWKPRQIDNPYKGTWHPHPEIDNPYSPDPSIYAYDN 310
Db 360 KCESAPGCGVMQRPMDNPNYKGVKWKPPMDNPNYQGLWPKPIPNPDFFEDLEPPQWTP 419
QY 311 FGVGLDLVQVSGTIFDNFLITNDEAYAEFGNETGVTKAAE-----KOMKDKQD 362
Db 420 FSAIGLELWSMTSDIFFDNFVCGDRRVDDWANDGMLKKAAGAAEPGVVGMQIEAAE 479
QY 363 E-----EORLKEEEDK-----KR 376
Db 480 ERPWLWVYVLTVALPVFLVISFCGSKGKQSPVEYKKTDAPOPDVKEEKEEEDKDG 539
QY 377 KEEBAEKEDDEDKDEEEDKEEEDKEEEDKEEEDKEEEDKEEEDKEEEDKEEEDKEEED 417
Db 540 DEEERKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEE 580
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RESULT 5

US-09-976-594-947
; Sequence 947, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT FILING DATE: 2001-10-12
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 947
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. 6673549 3876162CD1
US-09-976-594-947

Query Match 32.1%; Score 731.5; DB 4; Length 610;

Best Local Similarity 33.5%; Pred. No. 4.9e-58;
Matches 172; Conservative 82; Mismatches 135; Indels 125; Gaps 16;

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QY 21 VYKQFLDGDGWTSRWIESKHSD--FGKFLVSSGKPYGDEEK-----DKGLQTSQDA 72
Db 60 VYFAETP--DSRLAGWLVLSKAKDDMDDEISIIYDGRWEIEELKENOVDPGRGLVLSRA 117
QY 73 RPYALSASF--EPFSNKGQTLVVQFTVKEQNIIDCGGYVKLFPNSLD--QTMHGDSEYN 129
Db 118 KHAISAVLAKPFIADKPLIVQYEVNFQDIDCGGAYIKLLADTDDLLILENFYDKTSYI 177
QY 130 IMFGPDICGPTKVKVHVIENYKGNVLINKDIRCK-----DDEFTHLYTLIVRPD 179
Db 178 IMFGDKCKGB--DYKLHPIFRHKPKTGVFEKAKRPPDVLKXFFTDKTHLYTLVWNP 236
QY 180 NTYEVKIDNSQVSGSLEDW--DFLPPKIKPDASKPEDWDERAKIDDPDTSKPEDW- 236
Db 237 DTFEVLVQTVVNGSLLEDVVPKIPKPEIEDPNKKPSEWDERAKIPDPSAVKPEDWD 296
QY 237 -----DKPEHIPPDAKPEDWDEMDGEWEP-----262
Db 297 ESEPAQIEDSVVVPAGWLDDEPKFIPDPAEKPDWDEMDGEWEPQILNACRIGCG 356
QY 263 ---PVIONPEYKGEWKPRQIDNPYKGTWHPHPEIDNPYSPDPSIYAYDNFVGLDLW 319
Db 357 EWKPPMDNPNYKGVKWKPPMDNPNYQGLWPKPIPNPDFFEDLEPPQWTP 416
QY 320 QVKSQTIIDNLTNDEAYAEFGNETW-----GVTK-----AAE-----354
Db 417 SMTSDIYDFNFIISKEVADHWADGWKWKIMIANANKPGVLKQMAAEGHPWLWLIY 476
QY 355 -----KOMKDKQDEEQR-----LKEEEDKKEEEDKKEEEDKKEEEDKKEEED 380
Db 477 LVTAGVPIALITSCFWPRKVKKKHKDTYKKTDCIPQTKGVLEQKEEKEEKALEKPMOL 536
QY 381 BAEDKEDDED--KOEDREDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 412
Db 537 BEEKQNDGEMLEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEE 570
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RESULT 6

US-08-675-816-6
; Sequence 6, Application US/08675816
; Patent No. 6171864
; GENERAL INFORMATION:
; APPLICANT: Coughlan, Sean J.
; APPLICANT: Winfrey, Jr., Ron J.
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 701 Fifth Ave. Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675.816
; FILING DATE: 05-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6171864tenburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 750027.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)-622-4900
; TELEFAX: (206)-682-6031
; INFORMATION FOR SEQ ID NO: 6:

1 TDMHGDSEYNMFGPDICGPGTKKHVHVFNYKQNVLINKDIRCKDDEFTLHYTLVRPD 60

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US-08-930-114-3
; Sequence 3, Application US/08990114
; Patent No. 5932475
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Yue, Henry
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi

```



```

1 Sequence 2, Application US/08728323A
2
3 Patent No. 5948676
4 GENERAL INFORMATION:
5
6 APPLICANT: Chang, Yuan
7
8 APPLICANT: Bohenzky, Roy A.
9
10 APPLICANT: Russo, James J.
11
12 APPLICANT: Ebelman, Isidore S.
13
14 APPLICANT: Moore, Patrick S.
15
16 TITLE OF INVENTION: Immediate Early Protein From Kaposi's
17
18 TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
19
20 TITLE OF INVENTION: Encoding Same And Uses Thereof
21
22 NUMBER OF SEQUENCES: 21
23
24 CORRESPONDENCE ADDRESS:
25
26 ADDRESSEE: Cooper & Dunham LLP
27
28 STREET: 1185 Avenue of the Americas
29
30 CITY: New York
31
32 STATE: New York
33
34 COUNTRY: U.S.A.
35
36 ZIP: 10036
37
38 COMPUTER READABLE FORM:
39
40 MEDIUM TYPE: Floppy disk
41
42 COMPUTER: IBM PC Compatible
43
44 OPERATING SYSTEM: PC-DOS/MS-DOS
45
46 SOFTWARE: Patent In Release #1.0, Version #1.30
47
48 CURRENT APPLICATION DATA:
49
50 APPLICATION NUMBER: US/08/728,323A
51
52 FILING DATE:
53
54 CLASSIFICATION: 435
55
56 ATTORNEY/AGENT INFORMATION:
57
58 NAME: White, John F.
59
60 REGISTRATION NUMBER: 28,678
61
62 REFERENCE/DOCKET NUMBER: 0575/52268/JPW/MSC/SKS
63
64 TELECOMMUNICATION INFORMATION:
65
66 TELEPHONE: 212-278-0400
67
68 TELEFAX: 212-391-0525
69
70 INFORMATION FOR SEQ ID NO: 2:
71
72 SEQUENCE CHARACTERISTICS:
73
74 LENGTH: 1162 amino acids
75
76 TYPE: amino acid
77
78 TOPOLOGY: linear
79
80 MOLECULE TYPE: protein
81
82 PS-08-728-323A-2

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Query Match	7.7%	Score 175.5;	DB 2;	Length 1162;
Best Local Similarity	24.4%;	Pred. No. 4.8e-07;		
Matches 62;	Conservative 45;	Mismatches 88;	Indels 59;	Gaps 12;
203 LPPKIKDPASPEDWDERAKIDPT	---DSK----	---PEDWCKPEHI----	---PDPDAK	248
204 LPPKIKDPASPEDWDERAKIDPT	---DSK----	---PEDWCKPEHI----	---PDPDAK	248
134 LPP-----QRPPLSPTGPDSSITPMRPP	PPSQQTTPPHASPTTPPEPSPK	185		
249 KPED-----WDEWDGWEPP-----	PVTONPEY-----	KGKWKPROINDPY	285	
196 SSPDSLAPSTLRSLRKRRLSSQGPSTLN	LPICQSPVPPRCPDFANRSVVPWMATESPIY	245		
286 KGTWIHPEIDNPYSF-----	DPSIYAY--DNFGVLGLDLQWKSGTIFDNF	ITN	334	
246 VGS--SSDGGTTPRQPPTSPISIGSSP	SESGWGDDTAMLVLLAEIAEEASKNEKESCN	303		
335 DEAYAEFGNETGWGTVKAAEKQWKQ	QDBEQELKEEEDKRRKEEAEKDEDDKDED	394		
304 NQA--GEDNGNETSKESQVDKDNK	DNKDDEEBEQETDEECEEDEDDDEDDDEDDDE	362		
395 EDEEDKEEDEED	408			
363 EDEEDKEEDEED	376			

RESULT 14
US-09-298-568-2
; Sequence 2, Application US/09298568
; Patent No. 6322792
; GENERAL INFORMATION:

RESULT 13
US-08-728-323A-2

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2004, 12:50:22 ; Search time 46.2882 Seconds
(without alignments)
372.349 Million cell updates/sec

Title: US-09-807-148-5

Perfect score: 327

Sequence: 1 CGPGTKKHVIFNYKGNVL.....PDNTYEVKIDNSQVSGSL 61

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003ast.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	327	100.0	61	3	AA92352
2	327	100.0	180	3	AA92351
3	327	100.0	400	3	AA92350
4	327	100.0	401	2	AAW11156
5	327	100.0	416	7	ABE56306
6	327	100.0	416	7	ABE56310
7	327	100.0	417	1	AA92276
8	327	100.0	417	2	AA90927
9	327	100.0	417	3	AA92349
10	327	100.0	417	5	AAU7712
11	327	100.0	417	5	AAE24591
12	327	100.0	417	5	AAE18851
13	327	100.0	417	5	ABB82384
14	327	100.0	417	6	ABJ19766
15	327	100.0	417	6	ABG79824
16	327	100.0	417	6	ADA26337
17	327	100.0	417	7	ADD22407
18	327	100.0	417	7	AE56308
19	327	100.0	417	7	AE56312
20	318	97.2	60	3	AA92354
21	318	97.2	280	3	AA92355
22	280	85.6	403	2	AAW04171
23	278	85.0	406	4	ABE64414
24	258	78.9	49	3	AA92353
25	251	76.8	336	2	AA12312

26	190	58.1	122	2	AA900926
27	190	58.1	122	2	AA900924
28	186	56.9	415	4	AA66343
29	186	56.9	415	4	AA66341
30	185	56.6	419	7	ABM74155
31	184	56.3	385	3	ABM74155
32	184	56.3	390	6	ABO07134
33	182	55.7	122	2	AA900925
34	180	55.0	428	7	ABM74288
35	178	54.4	312	3	AA647933
36	178	54.4	312	3	AA647933
37	178	54.4	332	3	AA647933
38	178	54.4	421	3	AA647933
39	178	54.4	421	3	AA647933
40	178	54.4	424	3	AA647933
41	178	54.4	424	3	AA647933
42	178	54.4	441	3	AA647933
43	178	54.4	444	3	AA647933
44	170	52.0	420	5	ABB04656
45	117.5	35.9	592	4	ABB44554

ALIGNMENTS

RESULT 1

AA92352

ID AA92352 standard; protein; 61 AA.

XX

AC AA92352;

XX

DT 10-AUG-2000 (first entry)

XX

DE Recombinant human calreticulin residues 120-180.

XX

KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;

KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;

KW cytostatic; dermalogical; immunosuppressive; antiinflammatory; hepatic;

KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

XX Homo sapiens.

OS Synthetic.

XX

PN WO200020577-A1.

XX

PD 13-APR-2000.

XX

PF 05-OCT-1999; 99WO-US023240.

XX

PR 06-OCT-1998; 98US-0103438P.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Tosato G, Pike SE, Yao L;

XX

PP WPI; 2000-303767/26.

DR

PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,

XX

PS useful for suppressing tumor growth.

XX

PS Claim 4; Page 82-83; 99pp; English.

XX

CC A novel method of inhibiting endothelial cell growth comprises contacting the cells with calreticulin (or its fragments/variants). Fragments of calreticulin causes at least 40% inhibition of angiogenesis, tumor growth and/or endothelial cell growth (claimed). The method may be used for inhibiting angiogenesis in a patient. The angiogenesis is associated with a disease other than a tumor that is associated with neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiodermas, immune inflammation, atherosclerosis, excessive wound repair, retinal neovascularization, macular degeneration, corneal graft rejection, contact lens overwear, Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic

CC lupus erythromatosus, thyroiditis, Goodpasture's syndrome, systemic
 CC vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary
 CC biliary cirrhosis). The method may also be used for treating/inhibiting
 CC tumor growth especially Kaposi's sarcoma (claimed)
 XX SQ Sequence 61 AA;
 Query Match 100.0%; Score 327; DB 3; Length 61;
 Best Local Similarity 100.0%; Pred. No. 3.3e-38;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGPGTKKVHVFNYKGNVLINKDRCODEFTHLYTLVIRPDNTYEVKIDNSQVESGSL 60
 DB 1 CGPGTKKVHVFNYKGNVLINKDRCODEFTHLYTLVIRPDNTYEVKIDNSQVESGSL 60
 QY 61 E 61
 DB 61 E 61
 RESULT 2
 AAY92351
 ID AAY92351 standard; protein; 180 AA.
 XX AC AAY92351;
 XX DT 10-AUG-2000 (first entry)
 XX DE Human vasostatin (calreticulin N-terminal 180 amino acids).
 XX KW MBP-calreticulin; maltose binding protein; vasostatin; N-terminal;
 KW angiogenesis; inhibition; endothelial cell; anti-angiogenic;
 KW neuroprotective; antidiabetic; cytostatic; dermatological; hepatic;
 KW immunosuppressive; antiinflammatory; anti-atherosclerotic;
 KW gastrointestinal; anti-arthritis; ophthalmic.
 XX OS Homo sapiens.
 OS Synthetic.
 XX PN WO200020577-A1.
 XX PD 13-APR-2000.
 XX PF 05-OCT-1999; 99WO-US023240.
 XX PR 06-OCT-1998; 98US-0103438P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Tosato G, Pike SE, Yao L;
 XX DR WPI; 2000-303767/26.
 XX PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 XX useful for suppressing tumor growth.
 XX PS Claim 4; Page 82; 99pp; English.
 XX CC A novel method of inhibiting endothelial cell growth comprises contacting
 CC the cells with calreticulin (or its fragments/variants). Fragments of
 CC calreticulin causes at least 40% inhibition of angiogenesis, tumor growth
 CC and/or endothelial cell growth (claimed). The method may be used for
 CC inhibiting angiogenesis in a patient. The angiogenesis is associated with
 CC a disease other than a tumor that is associated with neovascularization
 CC (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular
 CC glaucoma, psoriasis, angiofibrosis, immune inflammation,
 CC atherosclerosis, excessive wound repair, retinal neovascularization,
 CC macular degeneration, corneal graft rejection, contact lens overwear,
 CC Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic
 CC lupus erythromatosus, thyroiditis, Goodpasture's syndrome, systemic
 CC vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary
 CC biliary cirrhosis). The method may also be used for treating/inhibiting
 CC tumor growth especially Kaposi's sarcoma (claimed)

XX SQ Sequence 180 AA;
 Query Match 100.0%; Score 327; DB 3; Length 180;
 Best Local Similarity 100.0%; Pred. No. 1.3e-37;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGPGTKKVHVFNYKGNVLINKDRCODEFTHLYTLVIRPDNTYEVKIDNSQVESGSL 60
 DB 120 CGPGTKKVHVFNYKGNVLINKDRCODEFTHLYTLVIRPDNTYEVKIDNSQVESGSL 179
 QY 61 E 61
 DB 180 E 180
 RESULT 3
 AAY92350
 ID AAY92350 standard; protein; 400 AA.
 XX AC AAY92350;
 XX DT 10-AUG-2000 (first entry)
 XX DE Recombinant human MBP-calreticulin.
 XX KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
 XX OS Homo sapiens.
 XX PN WO200020577-A1.
 XX PD 13-APR-2000.
 XX PF 05-OCT-1999; 99WO-US023240.
 XX PR 06-OCT-1998; 98US-0103438P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Tosato G, Pike SE, Yao L;
 XX DR WPI; 2000-303767/26.
 XX PR N-PSDB; AAA09346, AAA09347.
 XX PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 XX useful for suppressing tumor growth.
 XX PS Claim 4; Page 80-81; 99pp; English.
 XX CC Recombinant human MBP-calreticulin comprises the sequence of human
 CC calreticulin (see AAY92349) without the 17 N-terminal amino acids. A
 CC novel method of inhibiting endothelial cell growth comprises contacting
 CC the cells with calreticulin (or its fragments/variants). Fragments of
 CC calreticulin causes at least 40% inhibition of angiogenesis, tumor growth
 CC and/or endothelial cell growth (claimed). The method may be used for
 CC inhibiting angiogenesis in a patient. The angiogenesis is associated with
 CC a disease other than a tumor that is associated with neovascularization
 CC (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular
 CC glaucoma, psoriasis, angiofibrosis, immune inflammation,
 CC atherosclerosis, excessive wound repair, retinal neovascularization,
 CC macular degeneration, corneal graft rejection, contact lens overwear,
 CC Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic
 CC lupus erythromatosus, thyroiditis, Goodpasture's syndrome, systemic
 CC vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary
 CC biliary cirrhosis). The method may also be used for treating/inhibiting
 CC tumor growth especially Kaposi's sarcoma (claimed)
 XX SQ Sequence 400 AA;

Query Match 100.0%; Score 327; DB 3; Length 400;
 Best Local Similarity 100.0%; Pred. No. 3.8e-37; Indels 0; Gaps 0;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVHVFYFNKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSL 60
 |||||
 DB 120 CGPGTKKVHVFYFNKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSL 179
 |||||

QY 61 E 61
 DB 180 E 180

RESULT 4
 ID AAW11156 standard; peptide; 401 AA.
 XX AAW11156;
 AC AAW11156;
 XX AAW11156;
 DT 31-MAY-1997 (first entry)
 XX Calreticulin.
 DE Calreticulin.
 XX calreticulin; C-domain; restenosis; inhibitor.
 KW Homo sapiens.
 OS Homo sapiens.
 XX WO9636643-A1.
 FN 21-NOV-1996.
 XX 17-MAY-1996; 96WO-IB000471.
 XX 17-MAY-1996; 96US-00442844.
 PR 16-MAY-1996; 96US-00649417.
 XX (UYAL-) UNIV ALBERTA.
 PA Michalak M, Lucas A;
 PI WPI; 1997-012036/01.
 DR Inhibition of restenosis in patients - using calreticulin or a C-domain
 XX polypeptide of calreticulin or a variant with the same activity.
 PT Disclosure; Fig 1; 48pp; English.
 PS The present sequence is calreticulin. It and a C-domain derived peptide
 CC (AAW06736) are useful for treating a patient to inhibit restenosis. The
 CC calreticulin-type cpds. are administered either parenterally,
 CC intravenously or via a catheter and can target areas of vascular damage
 CC to inhibit or prevent restenosis
 XX Sequence 401 AA;
 SQ

Query Match 100.0%; Score 327; DB 2; Length 401;
 Best Local Similarity 100.0%; Pred. No. 3.8e-37; Indels 0; Gaps 0;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVHVFYFNKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSL 60
 |||||
 DB 120 CGPGTKKVHVFYFNKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSL 179
 |||||

QY 61 E 61
 DB 180 E 180

RESULT 5
 ID ADE56306 standard; protein; 416 AA.
 XX ADE56306;
 AC ADE56306;

XX 29-JAN-2004 (first entry)
 DT Rat Protein P18418, SEQ ID NO 2158.
 XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX Rattus norvegicus.
 OS WO2003016475-A2.
 PN 27-FEB-2003.
 XX 14-AUG-2002; 2002WO-US025765.
 PF 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX (GEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX Woolf C, D'urso D, Befort K, Costigan M;
 PI WPI; 2003-268312/26.
 DR GENBANK; P18418.
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 PS Claim 1; Page; 1017pp; English.
 XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 416 AA;
 SQ

Query Match 100.0%; Score 327; DB 7; Length 416;
 Best Local Similarity 100.0%; Pred. No. 4e-37; Indels 0; Gaps 0;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVHVFYFNKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSL 60
 |||||
 DB 137 CGPGTKKVHVFYFNKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSL 196
 |||||

QY 61 E 61
 DB 180 E 180

Db 197 E 197

RESULT 6
ADE56310
ID ADE56310 standard; protein; 416 AA.
XX
AC ADE56310;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein P18418, SEQ ID NO 2162.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P18418.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. Gene
CC injury (CCI) and spared nerve injury (SNI)).
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 416 AA;

Query Match 100.0%; Score 327; DB 7; Length 416;
Best Local Similarity 100.0%; Pred. No. 4e-37;

Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVHVIFNYKGNVINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVESGSL 60
Db 137 CGPGTKKVHVIFNYKGNVINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVESGSL 196
QY 61 E 61
Db 197 E 197

RESULT 7
AAP92276
ID AAP92276 standard; protein; 417 AA.
XX
AC AAP92276;
XX
DT 25-MAR-2003 (revised)
DT 23-FEB-1990 (first entry)
XX
DE 60 kD Ro (Ro/SSA) antigen.
XX
KW Sjorens syndrome; systemic lupus erythematosus.
XX
OS Synthetic.
XX
FN WO8909273-A.
XX
PD 05-OCT-1989.
XX
PF 22-MAR-1989; 89WO-US001213.
XX
PR 22-MAR-1988; 88US-00171634.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Sontheimer RD, Lieu TS, Capra JD, Mccaulliffe DP;
XX
DR WPI; 1989-309537/42.
DR N-PSDB; AAP92276.
XX
PT DNA sequences encoding antigenic epitope(s) of RO 60 KD auto-antigen -
PT used in immunoassays to detect rheumatic disease.
XX
PS Disclosure; Fig 2; 88pp; English.
XX
CC Synthetic peptides corresp. to an epitopic core of Ro antigen are
CC expressed recombinantly to detect autoantibodies, for identification of
CC autoimmune diseases. These epitopes are AAs 24-36, 23-36, 188-209, or 241
CC -255. The peptides may be substd. for ribonucleoprotein particle
CC antigens. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-
CC MAR-2003 to correct PI field.)
XX
SQ Sequence 417 AA;

Query Match 100.0%; Score 327; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 4e-37;

Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVHVIFNYKGNVINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVESGSL 60
Db 137 CGPGTKKVHVIFNYKGNVINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVESGSL 196
QY 61 E 61
Db 197 E 197

RESULT 8
AAY00927
ID AAY00927 standard; protein; 417 AA.
XX
AC AAY00927;


```
XX DT 28-MAY-1999 (first entry)
XX DE Calreticulin.
XX
XX Clq and collectin receptor; cC1qR binding domain; complement ubiquitin;
XX CUB functionality; inhibitor; complement activation; inflammation;
XX KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
XX KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
XX KW immune complex nephritis; therapy.
XX
XX OS Homo sapiens.
XX
XX WO9907406-A1.
XX
XX PD 18-FEB-1999.
XX
XX PF 12-AUG-1998; 98WO-GB002430.
XX
XX PR 12-AUG-1997; 97GB-00016998.
XX
XX (UYLE-) UNIV LEICESTER.
XX
XX PA Schwaeble W;
XX
XX PI WPI; 1999-180404/15.
XX
XX DR Use of a cC1qR binding domain - to modulate complement ubiquitin (CUB)
XX PT functionality.
XX
XX PS Disclosure; Page 26-27; 31pp; English.
XX
XX This sequence is calreticulin, a homologue of C1q and collectin receptor
XX (cC1qR). The invention relates to the use of a cC1qR binding domain in a
XX CC medicament to effect complement ubiquitin (CUB) functionality, and an
XX CC inhibitor of the cC1qR binding domain in a medicament to inhibit CUB
XX CC functionality. The cC1qR binding domain, or its inhibitor, can be used to
XX CC treat a human or animal body. Particularly an inhibitor is used to treat
XX CC complement activation involved in the initiation and maintenance of
XX CC inflammation, for example in myocardial infarction, brain ischaemia
XX CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus
XX CC erythematosus, burns, immune complex nephritis, and to treat amyloid
XX CC plaques in Alzheimer's disease. The use of cC1qR binding domain or
XX CC inhibitor enables the CUB domain functionality to be modulated using a
XX CC low molecular weight molecule
XX
XX SQ Sequence 417 AA;
XX
XX Query Match 100.0%; Score 327; DB 2; Length 417;
XX Best Local Similarity 100.0%; Pred. No. 4e-37;
XX Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 60
XX Db 137 CGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 196
XX
XX QY 61 E 61
XX Db 197 E 197
XX
XX RESULT 9
XX ID AA92349 standard; protein; 417 AA.
XX
XX AC AA92349;
XX
XX DT 10-AUG-2000 (first entry)
XX
XX DE Human MBP-calreticulin.
XX
XX KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
XX KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
```

```
KW cyostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Peptide 1..17
XX FT Protein /label= signal_peptide
XX FT 18 /label= mature_protein
XX
XX PN WO200020577-A1.
XX
XX PD 13-APR-2000.
XX
XX PF 05-OCT-1999; 99WO-US23240.
XX
XX PR 06-OCT-1998; 98US-0103438P.
XX
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Tosato G, Pike SE, Yao L;
XX
XX DR WPI; 2000-303767/26.
XX
XX N-PSDB; AAA09346, AAA09347.
XX
XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
XX PT useful for suppressing tumor growth.
XX
XX PS Disclosure; Page 79-80; 99pp; English.
XX
XX A novel method of inhibiting endothelial cell growth comprises contacting
XX the cells with calreticulin (or its fragments/variants). Fragments of
XX CC calreticulin causes at least 40% inhibition of angiogenesis, tumor growth
XX CC and/or endothelial cell growth (claimed). The method may be used for
XX CC inhibiting angiogenesis in a patient. The angiogenesis is associated with
XX CC a disease other than a tumor that is associated with neovascularization
XX CC (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular
XX CC glaucoma, psoriasis, angiofibromas, immune inflammation,
XX CC atherosclerosis, excessive wound repair, retinal neovascularization,
XX CC macular degeneration, corneal graft rejection, contact lens overwear,
XX CC Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic
XX CC lupus erythematosus, thyroiditis, Goodpasture's syndrome, systemic
XX CC vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary
XX CC biliary cirrhosis). The method may also be used for treating/inhibiting
XX CC tumor growth especially Kaposi's sarcoma (claimed)
XX
XX SQ Sequence 417 AA;
XX
XX Query Match 100.0%; Score 327; DB 3; Length 417;
XX Best Local Similarity 100.0%; Pred. No. 4e-37;
XX Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 60
XX Db 137 CGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 196
XX
XX QY 61 E 61
XX Db 197 E 197
XX
XX RESULT 10
XX ID AAU77712 standard; protein; 417 AA.
XX
XX AC AAU77712;
XX
XX DT 05-JUN-2002 (first entry)
XX
XX DE Human calreticulin (CRT).
XX
XX KW Calreticulin; CRT; endoplasmic reticulum chaperone polypeptide;
```

KW cytostatic; vaccine; human papillomavirus 16; HPV 16; E7; DNA vaccine;
 KW enhanced antigen-specific immune response; cytotoxic T lymphocyte;
 KW tumour; cancer; cervical cancer.
 XX
 OS Homo sapiens.
 XX WO200212281-A2.
 XX
 PN 14-FEB-2002.
 PD
 XX
 XX 02-AUG-2001; 2001WO-US024134.
 PF
 XX 03-AUG-2000; 2000US-0222902P.
 XX
 XX (UWJO) UNIV JOHNS HOPKINS.
 PA
 XX
 PI Wu T, Hung C;
 XX
 XX WPI; 2002-257463/30.
 DR N-PSDB; ABK11662.
 DR
 XX
 XX New nucleic acids encoding a fusion polypeptide comprising an endoplasmic
 PT reticulum chaperone polypeptide linked to an antigenic polypeptide,
 PT useful as a vaccine for inducing antigen-specific immune responses.
 XX
 XX Disclosure; Page 27; 71pp; English.
 PS
 XX The invention describes a nucleic acid molecule (I) encoding a fusion
 CC polypeptide comprising a first polypeptide domain comprising an
 CC endoplasmic reticulum chaperone polypeptide e.g. calreticulin (CRT) and a
 CC second polypeptide domain comprising at least one antigenic peptide e.g.
 CC Human papillomavirus 16 (HPV 16) E7. The nucleic acid is useful as a
 CC vaccine (DNA vaccine) for inducing enhanced antigen-specific immune
 CC responses, particularly those mediated by cytotoxic T lymphocytes. The
 CC nucleic acid and compositions comprising the nucleic acid is also useful
 CC for inhibiting the growth of tumours and cancers e.g. cervical cancer.
 CC This is the amino acid sequence of the human calreticulin (CRT), an
 CC endoplasmic reticulum protein used in the creation of a DNA vaccine
 XX
 SQ Sequence 417 AA;
 Query Match 100.0%; Score 327; DB 5; Length 417;
 Best Local Similarity 100.0%; Pred. No. 4e-37;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGPGTKKVVHVFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 60
 DB 137 CGPGTKKVVHVFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 196
 QY 61 E 61
 DB 197 E 197
 RESULT 11
 ID AAE24591 standard; protein; 417 AA.
 XX
 AC AAE24591;
 XX
 DT 04-OCT-2002 (first entry)
 XX
 DE Human calreticulin protein.
 XX
 KW Human; calreticulin; antisense compound; hyperproliferative disorder;
 KW cancer; autoimmune disease; viral infection; cardiovascular disease;
 KW antisense therapy; cytostatic; immunosuppressive; virucide.
 XX
 OS Homo sapiens.
 XX WO200236743-A2.
 PN
 XX 10-MAY-2002.
 PD

XX
 PF 30-OCT-2001; 2001WO-US049045.
 XX
 PR 30-OCT-2000; 2000US-00702327.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CF, Cowser LM;
 XX
 DR WPI; 2002-479759/51.
 DR N-PSDB; AAD39469.
 XX
 XX Novel antisense compound targeted to nucleic acid encoding calreticulin,
 PT useful for treating a human having disease or condition associated with
 PT calreticulin e.g. cancer, viral infection, autoimmune disease.
 XX
 PS Disclosure; Page 88-90; 109pp; English.
 CC
 CC The invention relates to antisense compounds, compositions and methods
 CC for modulating the expression of calreticulin. The compositions comprise
 CC antisense compounds, particularly antisense oligonucleotides, targeted
 CC to nucleic acids encoding calreticulin. The antisense compound is useful
 CC for inhibiting the expression of calreticulin in human cells or tissues.
 CC It is also useful for treating a human having a disease or condition
 CC associated with calreticulin, e.g., hyperproliferative disorder e.g.
 CC cancer, autoimmune disease, viral infection or cardiovascular disease, by
 CC inhibiting expression of calreticulin. It is useful for diagnostics,
 CC therapeutics, prophylaxis and as research reagents and kits. It is also
 CC used in antisense therapy. The present sequence is human calreticulin
 CC protein. This sequence is used in the exemplification of the invention
 XX
 SQ Sequence 417 AA;
 Query Match 100.0%; Score 327; DB 5; Length 417;
 Best Local Similarity 100.0%; Pred. No. 4e-37;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGPGTKKVVHVFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 60
 DB 137 CGPGTKKVVHVFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 196
 QY 61 E 61
 DB 197 E 197
 RESULT 12
 ID AAE18851 standard; protein; 417 AA.
 XX
 AC AAE18851;
 XX
 DT 17-MAY-2002 (first entry)
 XX
 DE Human calreticulin protein.
 XX
 KW Human; prostate cancer; calreticulin; T1D-1 protein; TRAITS protein;
 KW androgen action pathway; cell proliferation; kidney cancer; lymphoma;
 KW epithelium-derived carcinoma; leukaemia; vaccine; gene therapy;
 KW cytostatic; U19 protein.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 98..170
 FT /label= N-terminal_domain
 FT Region 98..103
 FT /label= Alpha_helix
 FT Region 149..154
 FT /label= Alpha_helix
 FT Domain 171..285
 FT /note= "Proline-rich domain (P domain)"
 FT Domain 286..397

FT XX /label= C-terminal_domain
PN WO200206327-A2.
XX 24-JAN-2002.
PD 17-JUL-2001; 2001WO-US022357.
XX 17-JUL-2000; 2000US-0218761P.
XX 16-JUL-2001; 2001US-00906393.
PR (NOUN) UNIV NORTHWESTERN.
XX Wang Z, Xiao W;
XX WPI; 2002-179780/23.
DR N-PSDB; AAD29931.
XX Identifying a subject that is likely to have aggressive form of prostate
PT cancer, involves comparing calreticulin levels in prostate specimen of
PT the subject and in benign prostatic epithelial cells of the same subject.
XX Disclosure; Page 146-148; 148pp; English.
XX The present invention relates to methods of distinguishing aggressive
CC forms of prostate cancer from non-aggressive forms. The method involves
CC comparing the level of calreticulin in prostate specimen and in benign
CC prostatic epithelial cells of a subject. The invention particularly
CC relates to two proteins, namely calreticulin and TID-1 (TRAITS; UI3) that
CC are down-regulated in aggressive forms of prostate cancer but not in
CC slowly progressing prostate cancer. They play important roles in the part
CC of androgen action pathway that suppresses cell proliferation and/or
CC prevents prostate cancer. The method is useful for identifying a subject
CC who is likely to have an aggressive form of prostate cancer. The
CC invention further relates to a method of identifying a subject with a
CC slow growing form of prostate cancer. TID-1 sequences are useful for
CC treating cancers such as epithelium-derived carcinomas, kidney cancers,
CC lymphomas, leukaemias and prostate cancers. Sequences of the invention
CC are used as vaccines and in gene therapy. The present sequence is human
CC calreticulin protein
XX
SQ Sequence 417 AA;
Query Match 100.0%; Score 327; DB 5; Length 417;
Best Local Similarity 100.0%; Pred. No. 4e-37;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGPGTKKVHVIFNYKGNVLINKDKDEFFTHLYTLIVRPDNTVEVKIDNSQVSGSL 60
Db 137 CGPGTKKVHVIFNYKGNVLINKDKDEFFTHLYTLIVRPDNTVEVKIDNSQVSGSL 196
QY 61 E 61
Db 197 E 197
RESULT 13
ABB82384
ID ABB82384 standard; protein; 417 AA.
XX ABB82384;
AC ABB82384;
DT 08-JAN-2003 (first entry)
XX Human calreticulin (CRT) protein.
DE
XX Immunogenicity; cytostatic; virucide; protozoacide; antibacterial; CTL;
KW hepatotropic; anti-HIV; vaccine. cytotoxic T lymphocyte; tumour; CRT;
KW Calreticulin; human.
XX Homo sapiens.
OS
XX WO200274920-A2.
PN

XX 26-SEP-2002.
PD 18-MAR-2002; 2002WO-US008033.
XX 16-MAR-2001; 2001US-0276854P.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Wu T, Hung C;
XX WPI; 2002-740856/80.
DR N-PSDB; ABV73173.
XX New nucleic acid molecule encoding an antigenic fusion polypeptide useful
PT as vaccines for enhancing or inducing immune responses, primarily
PT cytotoxic T lymphocytes (CTL) responses to specific antigens such as
PT tumor or viral antigens.
XX Disclosure; Page 27; 93pp; English.
XX The invention relates to a nucleic acid molecule that encodes a fusion
CC polypeptide, comprising a first nucleic acid sequence encoding a
CC polypeptide that comprises at least one immunogenicity-potentiating
CC polypeptide, optionally, fused in frame with the nucleic acid, a linker
CC nucleic acid encoding a linker peptide, and a nucleic acid that is linked
CC in frame to them, and that encodes an antigenic peptide or polypeptide.
CC The nucleic acid molecule, polypeptides and vectors are useful as
CC vaccines for enhancing immune responses, primarily cytotoxic T
CC lymphocytes (CTL) responses to specific antigens such as tumour or viral
CC antigens, and for inhibiting growth or preventing re-growth of a tumour.
CC The packaging cell line is useful for generating alphavirus replicon
CC particles without contamination from replicon-competent virus. The
CC pathogenic organisms include viruses such as human papilloma virus (HPV),
CC hepatitis B virus, hepatitis C virus, human immunodeficiency virus,
CC Epstein Barr virus and herpes simplex virus, intracellular parasites such
CC as malaria, and bacteria that grow intracellularly such as mycobacteria
CC and listeria. The present sequence represents a human calreticulin (CRT)
XX
SQ Sequence 417 AA;
Query Match 100.0%; Score 327; DB 5; Length 417;
Best Local Similarity 100.0%; Pred. No. 4e-37;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGPGTKKVHVIFNYKGNVLINKDKDEFFTHLYTLIVRPDNTVEVKIDNSQVSGSL 60
Db 137 CGPGTKKVHVIFNYKGNVLINKDKDEFFTHLYTLIVRPDNTVEVKIDNSQVSGSL 196
QY 61 E 61
Db 197 E 197
RESULT 14
ABB719766
ID ABB719766 standard; protein; 417 AA.
XX ABB719766;
AC ABB719766;
DT 03-APR-2003 (first entry)
XX Human MP21 protein CRTC SEQ ID No 46.
DE
XX Cytostatic; p21 pathway modulating agent; cancer; angiogenic; apoptotic;
KW cell proliferation disorder; MP21.
XX Homo sapiens.
OS
XX WO2003006990-A1.
PN 23-JAN-2003.
PD
XX

PF 10-JUL-2002; 2002WO-US021549.
 XX 12-JUL-2001; 2001US-0305017P.
 PR 10-OCT-2001; 2001US-0328491P.
 PR 15-FEB-2002; 2002US-0357452P.
 XX (EXEL-) EXELIXIS INC.
 PA
 XX
 XX
 PI Friedman L, Plowman GD, Belvin M, Li D, Funke RP;
 XX WPI: 2003-221779/21.
 DR N-PSDB; ABT17040.
 DR
 XX
 PT Identifying candidate p21 pathway modulator, by contacting an assay
 PT system having modifiers of p21 polypeptide or gene with a test agent to
 PT provide a reference activity in system and detecting test agent-biased
 PT activity.
 XX
 XX Example; Page 153-155; 199pp; English.
 PS
 XX
 CC The invention relates to a novel method for identifying a candidate p21
 CC pathway modulating agent. The novel method comprises contacting an assay
 CC system, comprising a purified p21 polypeptide (modifier of p21) or
 CC nucleic acid, with a test agent under conditions, so that but for the
 CC presence of a test agent, the assay system provides a reference activity
 CC and detection of test agent-biased activity of the assay system. The
 CC novel method of the invention is useful for identifying a candidate p21
 CC pathway modulating agent. The invention also includes a method for
 CC modulating the p21 pathway of a cell, and a method for diagnosing a
 CC disease e.g. cancer in a patient. The identified modulators are useful in
 CC diagnosis, therapy and pharmaceutical development. The modulators are
 CC useful in a variety of diagnostic and therapeutic applications including
 CC angiogenic, apoptotic and cell proliferation disorders. This sequence
 CC represents an MP21 protein of the invention
 XX
 SQ Sequence 417 AA;
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 Best Local Similarity 100.0%; Pred. No. 4e-37;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 60
 DB 137 CGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 196
 QY 61 E 61
 DB 197 E 197
 RESULT 15
 AAG79824
 ID AAG79824 standard; protein; 417 AA.
 AC
 XX
 XX AAG79824;
 DT 16-APR-2003 (first entry)
 XX
 XX Calreticulin.
 DE
 XX
 KW Motif; SE: signal transduction; Alzheimer's disease; neuronal cell;
 KW calreticulin; arrhythmia; idiopathic nephritic syndrome;
 KW non-autoimmune hyperthyroidism; obesity; polycystic kidney disease;
 KW cancer; asthma; atopic dermatitis; psoriasis; rheumatoid arthritis;
 KW systemic lupus erythematosus; infectious disease; atherosclerosis;
 KW inflammatory bowel disease; osteoarthritis; septic shock;
 KW congestive heart failure; insulin-resistance syndrome;
 KW ischaemia-reperfusion injury.
 XX
 OS Homo sapiens.
 XX
 PN WO200299061-A2.
 XX

PD 12-DEC-2002.
 XX 04-JUN-2002; 2002WO-US017536.
 XX 04-JUN-2001; 2001US-0295691P.
 PR 03-JUN-2002; 2002US-00161959.
 XX (UNMI) UNIV MICHIGAN.
 PA
 XX
 PI Holoshitz J, Ling S;
 XX WPI: 2003-156853/15.
 DR
 XX
 PT Treating diseases associated with signal transduction aberrations, e.g.
 PT Alzheimer's disease, arrhythmia or rheumatoid arthritis, comprises
 PT administering a preparation comprising an SE- or an SE motif-containing
 PT peptide.
 XX
 XX Disclosure; Fig 14; 97pp; English.
 PS
 XX
 CC This sequence represents human calreticulin. This protein was used in the
 CC method of the invention for treating diseases associated with signal
 CC transduction aberrations. The method comprises: (a) providing a subject
 CC with one or more symptoms of Alzheimer's disease and, optionally, a
 CC plurality of neuronal cells expressing calreticulin, and a preparation
 CC comprising an shared epitope (SE) - containing peptide or a peptide which
 CC binds the calreticulin; and (b) administering the preparation to the
 CC subject. The inventive method is useful for treating diseases associated
 CC with signal transduction aberrations, such as Alzheimer's disease,
 CC arrhythmia, idiopathic nephritic syndrome, non-autoimmune
 CC hyperthyroidism, obesity, polycystic kidney disease, cancer, asthma,
 CC atopic dermatitis, psoriasis, rheumatoid arthritis, systemic lupus
 CC erythematosus, infectious diseases, inflammatory bowel disease,
 CC osteoarthritis, septic shock, atherosclerosis, congestive heart failure,
 CC insulin-resistance syndrome, and ischaemia-reperfusion injury
 XX
 SQ Sequence 417 AA;
 Query Match 100.0%; Score 327; DB 6; Length 417;
 Best Local Similarity 100.0%; Pred. No. 4e-37;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 137 CGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 196
 QY 61 E 61
 DB 197 E 197
 Search completed: October 4, 2004, 13:03:31
 Job time : 48.2882 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2004, 13:01:22 ; Search time 13.6353 Seconds
(without alignments)
230.958 Million cell updates/sec

Title: US-09-807-148-5

Perfect score: 327

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	327	100.0	180	4	US-09-828-000-3
3	327	100.0	416	4	US-09-828-000-2
4	244	74.6	61	4	US-09-828-000-4
5	189	57.8	35	4	US-09-828-000-7
6	186	56.9	415	3	US-08-675-816-2
7	151	46.2	27	4	US-09-828-000-5
8	115.5	35.3	593	1	US-08-296-362-2
9	107.5	32.9	610	4	US-09-976-594-947
10	96	29.4	18	4	US-09-828-000-6
11	82.5	25.2	542	3	US-08-675-816-5
12	61.5	18.8	582	3	US-08-906-865-3
13	61.5	18.8	582	4	US-09-129-668-3
14	57.5	17.6	126	4	US-09-732-210-1163
15	55	16.8	588	4	US-09-252-991A-18861
16	54.5	16.7	410	2	US-08-723-415B-10
17	54.5	16.7	410	3	US-09-189-627A-10
18	54.5	16.7	410	4	US-09-710-861-10
19	54	16.5	405	1	US-07-829-954-2
20	54	16.5	405	1	US-07-994-423-2
21	54	16.5	405	1	US-08-421-891-2
22	54	16.5	474	4	US-09-134-001C-3176
23	54	16.5	816	1	US-08-190-802A-54
24	54	16.5	816	3	US-08-477-346-54
25	54	16.5	816	4	US-08-473-089-54
26	54	16.5	816	4	US-08-487-072A-54
27	54	16.5	1009	4	US-09-693-146-4

28 53.5 16.4 279 2 US-08-701-191A-23 Sequence 23, Appl
29 53.5 16.4 279 4 US-09-564-526-23 Sequence 23, Appl
30 53.5 16.4 355 1 US-08-322-549-6 Sequence 6, Appl
31 53.5 16.4 355 3 US-09-006-353A-14 Sequence 14, Appl
32 53.5 16.4 355 4 US-09-573-986-14 Sequence 14, Appl
33 53.5 16.4 812 1 US-08-446-794A-4 Sequence 4, Appl
34 53.5 16.4 943 4 US-09-540-236-3458 Sequence 3458, Ap
35 53.5 16.4 984 2 US-08-673-789-9 Sequence 9, Appl
36 53.5 16.4 984 2 US-08-449-645A-19 Sequence 19, Appl
37 53.5 16.4 984 2 US-08-702-367A-19 Sequence 19, Appl
38 53.5 16.4 984 5 PCT-US95-04681-19 Sequence 19, Appl
39 53 16.2 91 4 US-09-134-001C-2369 Sequence 2369, Ap
40 53 16.2 410 2 US-08-723-415B-11 Sequence 11, Appl
41 53 16.2 410 2 US-08-428-131-2 Sequence 2, Appl
42 53 16.2 410 3 US-08-602-846-2 Sequence 2, Appl
43 53 16.2 410 3 US-09-078-596-2 Sequence 2, Appl
44 53 16.2 410 3 US-09-189-627A-11 Sequence 11, Appl
45 53 16.2 410 4 US-09-710-861-11 Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-828-000-8
; Sequence 8, Application US/09828000
; Patent No. 6596890
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Fragment 5
US-09-828-000-8

Query Match 100.0%; Score 327; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 2.5e-37;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGPGTKKVHVFYNYKGNVLINKDIRCKDDEFTLYTLIVRPDNTYEVKIDNSQVESGSL 60
Db 1 CGPGTKKVHVFYNYKGNVLINKDIRCKDDEFTLYTLIVRPDNTYEVKIDNSQVESGSL 60
Qy 61 E 61
Db 61 E 61

RESULT 2
US-09-828-000-3
; Sequence 3, Application US/09828000
; Patent No. 6596890
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Vasostatin
US-09-828-000-3
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Dd	120	CSPGPKYHVLFNFKGVNLINKDIRCKDDEFFHLTYLIVRPDNTVEVVDINSQVESASGL	179									
Qy	61	E	61									
Dd	180	F	180									

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RESULT 3
US-09-828-000-2
; Sequence 2, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Calreticulin
US-09-828-000-2

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RESULT 4
US-09-828-000-4
; Sequence 4, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Fragment 1
US-09-828-000-4

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RESULT 5
US-09-828-000-7
; Sequence 7, Application US/09828000

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; Patent No. 6596690
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; GENERAL INFORMATION:
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; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Fragment 4
; US-09-828-000-7

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RESULT 6
US-08-675-816-2
; Sequence 2, Application US/08675816
; Patent No. 6171864
; GENERAL INFORMATION:
; APPLICANT: Coughlan, Sean J.
; APPLICANT: Winfrey, Jr., Ron J.
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 701 Fifth Ave. Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,816
; FILING DATE: 05-JUL-1996

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RESULT 7
US-09-828-000-5
; Sequence 5, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Fragment 2
; US-09-828-000-5

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Db 1 CGPGTKKVHVIFNYKGNVLINKDIRC 27

RESULT 8
US-08-296-362-2
; Sequence 2, Application US/08296362
; Patent No. 5691306
; GENERAL INFORMATION:
; APPLICANT: Bergeron, John J.M.
; APPLICANT: Thomas, David Y.
; APPLICANT: Wada, Ikuro
; TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF
; TITLE OF INVENTION: PROTEIN TRAFFICKING DISORDERS AND INCREASING SECRETORY
; TITLE OF INVENTION: PROTEIN PRODUCTION
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SEED and BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/296,362
; FILING DATE: 25-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deehr, Manya S.
; REGISTRATION NUMBER: 37,120
; REFERENCE/DOCKET NUMBER: 690066.401C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 593 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-296-362-2

Query Match      35.3%; Score 115.5; DB 1; Length 593;
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Qy 51 DNSQVESGSL 60
Db 254 DOSIVNSGNL 263

RESULT 9
US-09-976-594-947
; Sequence 947, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 947
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. 6673549 3876162CD1
; US-09-976-594-947

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Qy 51 DNSQVESGSL 60
Db 244 DOTVVNGSL 253

RESULT 10
US-09-828-000-6
; Sequence 6, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Fragment 3
; US-09-828-000-6

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Qy 10 VIFNYKGNVLINKDIRC 27
Db 1 VIFNYKGNVLINKDIRC 18
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; APPLICANT: Liang, Jihong
; APPLICANT: Mittanck, Cindy A.
; APPLICANT: Seale, Jeffrey W.
; APPLICANT: Wu, Yonnie S.
; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
; FILE REFERENCE: 38-21(15036)B
; CURRENT APPLICATION NUMBER: US/09/732,210
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,513
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: US 60/169,340
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 1753
; SEQ ID NO 1163
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Porphyra purpurea
US-09-732-210-1163

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DB 10 PNKRIEIALTYIGIGLSRSKEILKKTINIDADIRQNLNDQQIVSIREIL---ESSYQI 66
QY 49 KIDNSQVESGSL 61
DB 67 EGDLEKRFESMSIK 79

RESULT 15
US-09-252-991A-18861
; Sequence 18861, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18861
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18861

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DB 364 RGDPLGKDIRKLDVDDVLYTAL 388

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Job time : 14.6353 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

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Run on: October 4, 2004, 13:06:03 ; Search time 44.8529 Seconds
(without alignments)
437.647 Million cell updates/sec

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Scoring table: BLOSUM62
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Post-processing: Minimum Match 0%
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Database : Published Applications AA:*

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- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	327	100.0	61	15	US-10-405-588-8
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5	327	100.0	416	10	US-09-828-000-2
6	327	100.0	416	14	US-10-316-253-2
7	327	100.0	416	14	US-10-316-253-4
8	327	100.0	416	14	US-10-316-253-6
9	327	100.0	416	15	US-10-405-588-2
10	327	100.0	417	10	US-09-906-393A-36
11	327	100.0	417	14	US-10-161-959-29
12	327	100.0	417	15	US-10-367-093-14
13	244	74.6	61	10	US-09-828-000-4
14	244	74.6	61	15	US-10-405-588-4
15	219.5	67.1	395	15	US-10-369-493-6343

Query Match 100.0%; Score 327; DB 10; Length 61;
Best Local Similarity 100.0%; Pred. No. 1.2e-35;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDKCKDETHLYTLVRPONTVEVKIDNSQVESGSL 60
Db 1 CGPGTKKHVIFNYKGNVLINKDKCKDETHLYTLVRPONTVEVKIDNSQVESGSL 60

QY 61 E 61

Db 61 E 61

RESULT 2

US-10-405-588-8
; Sequence 8, Application US/10405588
; Publication No. US20030216229A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant

213 65.1 210 16 US-10-767-701-55877
189 57.8 35 10 US-09-828-000-7
18 35 15 US-10-405-588-7
19 346 12 US-10-425-114-48930
20 188 57.5 421 16 US-10-767-701-46544
21 188 57.5 435 12 US-10-425-114-70304
22 188 57.5 442 16 US-10-437-963-114914
23 188 57.5 667 16 US-10-437-963-114860
24 186 56.9 388 12 US-10-425-114-46405
25 186 56.9 391 12 US-10-425-114-69619
26 186 56.9 442 12 US-10-425-114-46869
27 185 56.6 290 12 US-10-425-114-44768
28 185 56.6 422 12 US-10-424-599-277445
29 184 56.3 390 15 US-10-161-927-46
30 183 56.0 425 16 US-10-437-963-122222
31 180 55.0 391 12 US-10-424-599-190956
32 180 55.0 391 12 US-10-425-114-46228
33 180 55.0 391 12 US-10-425-114-55995
34 180 55.0 420 12 US-10-424-599-190958
35 180 55.0 434 16 US-10-437-963-201427
36 180 55.0 434 12 US-10-425-114-70140
37 180 55.0 439 12 US-10-425-114-65495
38 179 54.7 247 12 US-10-424-599-153809
39 179 54.7 372 12 US-10-425-114-44821
40 179 54.7 372 12 US-10-425-114-54997
41 179 54.7 418 12 US-10-424-599-153808
42 179 54.7 424 16 US-10-437-963-201420
43 175 53.5 279 16 US-10-767-701-39041
44 175 53.5 422 16 US-10-767-701-45264
45 175 53.5 431 16 US-10-767-701-44015

ALIGNMENTS

RESULT 1
US-09-828-000-8
; Sequence 8, Application US/09828000
; Publication No. US20030078198A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Fragment 5
US-09-828-000-8

Query Match 100.0%; Score 327; DB 10; Length 61;
Best Local Similarity 100.0%; Pred. No. 1.2e-35;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDKCKDETHLYTLVRPONTVEVKIDNSQVESGSL 60
Db 1 CGPGTKKHVIFNYKGNVLINKDKCKDETHLYTLVRPONTVEVKIDNSQVESGSL 60

QY 61 E 61

Db 61 E 61

RESULT 2

US-10-405-588-8
; Sequence 8, Application US/10405588
; Publication No. US20030216229A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant

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; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/10/405,588
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US/09/828,000
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Fragment 5
US-10-405-588-8

Query Match
Best Local Similarity 100.0%; Score 327; DB 15; Length 61;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHLTYTLIVRPDNTYEVKIDNSQVESGSL 60
Db 1 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHLTYTLIVRPDNTYEVKIDNSQVESGSL 60
QY 61 E 61
Db 61 E 61

RESULT 3
US-09-828-000-3
; Sequence 3, Application US/09828000
; Publication No. US20030078198A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Vasostatin
US-09-828-000-3

Query Match
Best Local Similarity 100.0%; Score 327; DB 10; Length 180;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHLTYTLIVRPDNTYEVKIDNSQVESGSL 60
Db 120 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHLTYTLIVRPDNTYEVKIDNSQVESGSL 179
QY 61 E 61
Db 180 E 180

RESULT 4
US-10-405-588-3
; Sequence 3, Application US/10405588
; Publication No. US20030216299A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/10/405,588
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US/09/828,000
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-2

Query Match
100.0%; Score 327; DB 14; Length 416;
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; TYPE: PRT
; ORGANISM: Vasostatin
US-10-405-588-3

Query Match
100.0%; Score 327; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 4.8e-35;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHLTYTLIVRPDNTYEVKIDNSQVESGSL 60
Db 120 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHLTYTLIVRPDNTYEVKIDNSQVESGSL 179
QY 61 E 61
Db 180 E 180

RESULT 5
US-09-828-000-2
; Sequence 2, Application US/09828000
; Publication No. US20030078198A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Calreticulin
US-09-828-000-2

Query Match
100.0%; Score 327; DB 10; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.4e-34;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHLTYTLIVRPDNTYEVKIDNSQVESGSL 60
Db 137 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHLTYTLIVRPDNTYEVKIDNSQVESGSL 196
QY 61 E 61
Db 197 E 197

RESULT 6
US-10-316-253-2
; Sequence 2, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-2

Query Match
100.0%; Score 327; DB 14; Length 416;
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Best Local Similarity 100.0%; Pred. No. 1.4e-34;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 60
DB 137 CGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 196

QY 61 E 61

DB 197 E 197

RESULT 7

US-10-316-253-4
; Sequence 4, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-4

Query Match 100.0%; Score 327; DB 14; Length 416;

Best Local Similarity 100.0%; Pred. No. 1.4e-34;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 60
DB 137 CGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 196

QY 61 E 61

DB 197 E 197

RESULT 8

US-10-316-253-6
; Sequence 6, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-6

Query Match 100.0%; Score 327; DB 14; Length 416;

Best Local Similarity 100.0%; Pred. No. 1.4e-34;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 327; DB 14; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.4e-34;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 60
DB 137 CGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 196

QY 61 E 61

DB 197 E 197

RESULT 9

US-10-405-588-2
; Sequence 2, Application US/10405588
; Publication No. US20030216299A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/10/405,588
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US/09/828,000
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Calreticulin
US-10-405-588-2

Query Match 100.0%; Score 327; DB 15; Length 416;

Best Local Similarity 100.0%; Pred. No. 1.4e-34;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 60
DB 137 CGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 196

QY 61 E 61

DB 197 E 197

RESULT 10

US-09-906-393A-36
; Sequence 36, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-393A-36

Query Match 100.0%; Score 327; DB 10; Length 417;

Best Local Similarity 100.0%; Pred. No. 1.4e-34;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 60
DB 137 CGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 196

QY 61 E 61

DB 197 E 197

Db 137 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 196

Qy 61 E 61

Db 197 E 197

RESULT 11

US-10-161-959-29
; Sequence 29, Application US/10161959
; Publication No. US2003009674A1
; GENERAL INFORMATION:
; APPLICANT: Holoshitz, Joseph
; TITLE OF INVENTION: Methods and Compositions for the Treatment of Diseases Associated
; FILE REFERENCE: UM-07135
; CURRENT APPLICATION NUMBER: US/10/161,959
; CURRENT FILING DATE: 2002-10-01
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-161-959-29

Query Match 100.0%; Score 327; DB 14; Length 417;

Best Local Similarity 100.0%; Pred. No. 1.4e-34;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 60

Db 137 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 196

Qy 61 E 61

Db 197 E 197

RESULT 12

US-10-367-093-14
; Sequence 14, Application US/10367093
; Publication No. US20030216315A1
; GENERAL INFORMATION:
; APPLICANT: Duke University
; APPLICANT: Nicchitta, Chris
; APPLICANT: Baker-LePain, Julie
; TITLE OF INVENTION: MODULATION OF IMMUNE RESPONSE BY NON-PEPTIDE BINDING STRESS RESPO
; FILE REFERENCE: 180/145
; CURRENT APPLICATION NUMBER: US/10/367,093
; CURRENT FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-093-14

Query Match 100.0%; Score 327; DB 15; Length 417;

Best Local Similarity 100.0%; Pred. No. 1.4e-34;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 60

Db 137 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 196

Qy 61 E 61

Db 197 E 197

RESULT 13

US-09-828-000-4
; Sequence 4, Application US/09828000
; Publication No. US20030078198A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Fragment 1
US-09-828-000-4

Query Match 74.6%; Score 244; DB 10; Length 61;

Best Local Similarity 100.0%; Pred. No. 1.2e-24;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDN 44

Db 18 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDN 61

RESULT 14

US-10-405-588-4
; Sequence 4, Application US/10405588
; Publication No. US20030216299A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/10/405,588
; CURRENT FILING DATE: 2003-04-01
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Fragment 1
US-10-405-588-4

Query Match 74.6%; Score 244; DB 15; Length 61;

Best Local Similarity 100.0%; Pred. No. 1.2e-24;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDN 44

Db 18 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDN 61

RESULT 15

US-10-369-493-6343
; Sequence 6343, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

Mon Oct 4 14:24:05 2004

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; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6343
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6343

Query Match      67.1%; Score 219.5; DB 15; Length 395;
Best Local Similarity 67.2%; Pred. No. 2.4e-20;
Matches 41; Conservative 12; Mismatches 12; Indels 1; Gaps 1;

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Db      133 CGP-TRRVHVILNYKGENKLKKEITCKSDELTHLYTLILNSDNTYEVKIDGESACTGSL 191

QY      61 E 61
Db      192 E 192
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Search completed: October 4, 2004, 13:17:33
Job time : 45.8529 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2004, 12:55:52 ; Search time 13.2765 Seconds
(without alignments)
441.961 Million cell updates/sec

Title: US-09-807-148-5

Perfect score: 327

Sequence: 1 CGPGTKKHVIFNYKGNVL.....PDNTYEVKIDNSQVESGSL 61

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR78:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	327	100.0	416	1 S06763	calreticulin precu
2	327	100.0	416	2 JH0819	calreticulin precu
3	327	100.0	417	1 A37047	calreticulin precu
4	327	100.0	418	1 A34154	calreticulin precu
5	322	98.5	400	2 S43376	calreticulin, brai
6	322	98.5	421	2 S63799	calreticulin precu
7	280	88.7	405	1 JH0795	calreticulin precu
8	287	87.8	384	2 S29130	calreticulin (clon
9	287	87.8	411	2 S29129	calreticulin precu
10	278	85.0	406	2 A56637	calreticulin homol
11	271	82.9	419	2 S71343	calreticulin precu
12	251	76.8	336	2 A32507	41K larval antigen
13	236	72.2	393	1 A48573	calreticulin autoa
14	219.5	67.1	395	2 S25851	calreticulin precu
15	193	59.0	416	2 T44554	calreticulin - bee
16	188	57.5	421	2 S58170	calreticulin precu
17	186	56.9	415	2 T01072	calreticulin - cas
18	185	56.6	412	2 T05703	calreticulin - bar
19	185	56.6	415	2 T05705	calreticulin (Crt1
20	181	55.4	425	2 C96605	calreticulin - com
21	178	54.4	389	2 T03691	calreticulin call
22	178	54.4	416	2 T06968	calreticulin call
23	178	54.4	444	2 H86224	hypothetical prote
24	177	54.1	422	2 T07841	probable calreticu
25	117.5	35.9	592	2 I53260	calnexin - human
26	117.5	35.9	592	2 A46673	calnexin precursor
27	116.5	35.6	591	2 B54354	calnexin precursor
28	116.5	35.6	591	2 C54354	calnexin precursor
29	115.5	35.3	593	1 A37273	calnexin precursor

30	114.5	35.0	582	2 A46637	calnexin homolog S
31	109.5	33.5	622	2 S71342	calnexin precursor
32	106.5	32.6	611	2 A53448	calnexin precursor
33	106.5	32.6	611	2 A54086	calnexin-t - mouse
34	101.5	31.0	619	2 S40938	hypothetical prote
35	99	30.3	560	2 S56142	calcium-binding pr
36	90.5	27.7	546	2 T06415	calnexin - soybean
37	88.5	27.1	297	2 S70552	calnexin homolog C
38	85.5	26.1	530	2 JN0597	calnexin-like prot
39	84	25.7	356	2 A46164	calnexin - human
40	80.5	24.6	540	2 T10892	probable calnexin
41	78.5	24.0	428	2 T03251	calnexin - maize
42	75.5	23.1	532	2 T49873	calnexin homolog
43	73.5	22.5	540	1 J00470	site-specific DNA-
44	64.5	19.7	981	2 T46330	hypothetical prote
45	64	19.6	451	2 T16162	hypothetical prote

ALIGNMENTS

RESULT 1

S06763
calreticulin precursor - mouse
N:Alternate names: S5K calcium-binding reticuloplasmin; calregulin
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S06763; J01444; F01233; A57498
R:Smith, M.J.; Koch, G.L.E.
EMBO J. 8, 3581-3586, 1989
A:Title: Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a m
A:Reference number: S06763; MUID:90059955; PMID:2583110
A:Accession: S06763
A:Molecule type: DNA
A:Residues: 1-416 <SMT>
A:Cross-references: ENBL:X14926; NID:G50567; PIDN:CAA33053.1; PID:G50568
R:Mazarella, R.A.; Gold, P.; Cunningham, M.; Green, M.
Gene 120, 217-225, 1992
A:Title: Determination of the sequence of an expressible cDNA clone encoding ERp60/calr
A:Reference number: J01444; MUID:93013037; PMID:1398135
A:Accession: J01444
A:Molecule type: mRNA
A:Residues: 1-416 <MAZ>
A:Cross-references: GB:M2988; NID:G193084; PIDN:AAA37569.1; PID:G193085
A:Accession: P01233
A:Molecule type: protein
A:Residues: 18-41 <MA2>
R:White, T.K.; Zhu, Q.; Tanzer, M.L.
J. Biol. Chem. 270, 15928-15929, 1995
A:Title: Cell surface calreticulin is a putative mannoside lectin which triggers mouse
A:Reference number: A57498; MUID:95332280; PMID:7608143
A:Accession: A57498
A>Status: preliminary
A:Molecule type: protein
A:Residues: 74-80;142-151;186-193 <WHI>
C:Superfamily: calreticulin
C:Keywords: calcium binding
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-416/Product: calregulin #status experimental <MA1>
F:413-416/Region: endoplasmic reticulum retention signal

```

A:Accession: A57498
A>Status: preliminary
A:Molecule type: protein
A:Residues: 74-80|142-151;186-193 <WHI>
C:Superfamily: calreticulin
C:Keywords: calcium binding
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-416/Product: calregulin #status experimental <WAT>
F:413-416/Region: endoplasmic reticulum retention signal

Query Match          100.0%; Score 327; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.4e-30;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

JH0819
 calreticulin precursor - rat
 N:Alternate names: calcium-binding protein 3
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Jun-2000
 C:Accession: JH0819; A49176; S11205; PC1109; S45036; S04867; S39372; A34473; S13045
 R:Nakamura, M.; Moriya, M.; Baba, T.; Michikawa, Y.; Yamanobe, T.; Arai, K.; Okinaga, S.
 Exp. Cell Res. 205, 101-110, 1993
 A:Title: An endoplasmic reticulum protein, calreticulin, is transported into the acrosome
 A:Reference number: A49176; MUID:93202172; PMID:8453984
 A:Accession: JH0819
 A:Molecule type: mRNA
 A:Residues: 1-416 <NAK>
 A:Cross-references: GB:D78308; NID:g1089798; PIDN:BAAL11345.1; PID:g1845572
 A:Accession: A49176
 A>Status: preliminary
 A:Molecule type: mRNA; protein
 A:Residues: 1-416 <NA2>
 A:Cross-references: GB:D78308; NID:g1089798; PIDN:BAAL11345.1; PID:g1845572
 A:Experimental source: Sprague-Dawley, spermatogenic cells
 A>Note: sequence extracted from NCBI backbone (NCBIN:127639, NCBIIP:127643)
 R:Murthy, K.K.; Banville, D.; Srikant, C.B.; Carrier, F.; Holmes, C.; Bell, A.; Patel, Y.
 Nucleic Acids Res. 18, 4933, 1990
 A:Title: Structural homology between the rat calreticulin gene product and the Onchocerca
 A:Reference number: S11205; MUID:90370496; PMID:2395861
 A:Accession: S11205
 A:Molecule type: mRNA
 A:Residues: 1-416 <MUR>
 A:Cross-references: EMBL:X53363; NID:g55854; PIDN:CRAA37446.1; PID:g55855
 R:Nakamura, M.; Michikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.
 Biochem. Biophys. Res. Commun. 166, 668-673, 1992
 A:Title: Calreticulin is present in the acrosome of spermatozoa of rat testis.
 A:Reference number: PC1109; MUID:92360010; PMID:1497655
 A:Accession: PC1109
 A:Molecule type: protein
 A:Residues: 18-32 <NAK2>
 A:Experimental source: testis, strain Sprague-Dawley
 R:Soennichsen, B.; Fueflekrug, J.; van Nguyen, P.; Diekmann, W.; Robinson, D.G.; Mieskes
 submitted to the EMBL Data Library, May 1994
 A:Description: Retention and retrieval: both mechanisms cooperate to maintain calreticulin
 A:Reference number: S45036
 A:Accession: S45036
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-416 <SOE>
 A:Cross-references: EMBL:X79327; NID:g488840; PIDN:CAA55890.1; PID:g488841
 R:Lone, Y.C.; Bailly, A.; Latruffe, N.
 submitted to the EMBL Data Library, December 1988
 A:Reference number: S04867
 A:Accession: S04867
 A:Molecule type: mRNA
 A:Residues: 'R', 270-358, 'AAG', <LON>
 A:Cross-references: EMBL:X13702; NID:g56055; PIDN:CAA31987.1; PID:g930260
 A>Note: the authors designated the protein as D-beta-hydroxyputyrate dehydrogenase
 R:Yokoi, T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horiuchi, R.; Kamataki, T.
 Biochim. Biophys. Acta 1158, 339-344, 1993
 A:Title: Identification of protein disulfide isomerase and calreticulin as autoimmure an
 A:Reference number: S39371; MUID:94072621; PMID:8251535
 A:Accession: S39372
 A:Molecule type: protein
 A:Residues: 18-23 'X', 25-32 <YOK>
 R:Van, P.N.; Peter, F.; Seeling, H.D.
 J. Biol. Chem. 264, 17494-17501, 1989
 A:Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes with
 itive calcium sequestering rat liver vesicles.
 A:Reference number: A34473; MUID:90008920; PMID:2793869
 A:Accession: A34473
 A>Status: preliminary
 A:Molecule type: Protein
 A:Residues: 18-36 <VAN>
 R:Treves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meld

Biochem. J. 271, 473-480, 1990
 A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage
 A:Reference number: S13045; MUID:91054414; PMID:2241926
 A:Accession: S13045
 A:Molecule type: protein
 A:Residues: 18-29 <TRE>
 C:Superfamily: calreticulin
 C:Keywords: calcium binding; glycoprotein
 F:1-17/Domain: signal sequence
 F:18-416/Product: calreticulin #status predicted <SIG>
 F:204-212/Region: nuclear location signal
 F:413-416/Region: endoplasmic reticulum retention signal
 F:344/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 100.0%; Score 327; DB 2; Length 416;
 Best Local Similarity 100.0%; Pred. NO. 1.4e-30;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGPOTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEKIDNSQVSGSL 60
 DB 137 CGPOTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEKIDNSQVSGSL 196
 QY 61 E 61
 DB 197 E 197
 RESULT 3
 A37047
 calreticulin precursor - human
 N:Alternate names: 52K ribonucleoprotein autoantigen Ro/SS-A; 60K integrin-binding prote
 C:Species: Homo sapiens (man)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Feb-2000
 C:Accession: A42330; A37047; A46452; A28812; A40346; S11475; T45075
 R:McCaulliffe, D.P.; Yang, Y.S.; Wilson, J.; Sontheimer, R.D.; Capra, J.D.
 J. Biol. Chem. 267, 2557-2562, 1992
 A:Title: The 5'-flanking region of the human calreticulin gene shares homology with the
 A:Reference number: A42330; MUID:92129342; PMID:1733953
 A:Accession: A42330
 A:Molecule type: DNA
 A:Residues: 1-417 <MC2>
 A>Note: sequence extracted from NCBI backbone (NCBIN:78537, NCBIIP:78536)
 R:McCaulliffe, D.P.; Lux, F.A.; Lieu, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachinski
 J. Clin. Invest. 85, 1379-1391, 1990
 A:Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/SS-
 A:Reference number: A37047; MUID:90237213; PMID:2332496
 A:Accession: A37047
 A:Molecule type: mRNA
 A:Residues: 1-417 <MCC>
 A:Cross-references: GB:M32294; NID:g337486; PIDN:AAA36582.1; PID:g337487
 A>Note: the authors translated the codon GTA for residue 349 as Tyr
 R:Rokeach, J.A.; Haseib, J.A.; Mellof, J.F.; Smeenk, R.J.; Unnasch, T.R.; Greene, B.M.;
 J. Immunol. 147, 3031-3039, 1991
 A:Title: Characterization of the autoantigen calreticulin.
 A:Reference number: A46452; MUID:92013129; PMID:1919005
 A:Accession: A46452
 A:Molecule type: mRNA
 A:Residues: 1-417 <ROK>
 A:Cross-references: GB:M84739; NID:g179881; PIDN:AAA51916.1; PID:g179882
 A>Note: sequence extracted from NCBI backbone (NCBIN:60749, NCBIIP:60750)
 R:Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sontheimer, R.D.
 J. Clin. Invest. 82, 96-101, 1988
 A:Title: Molecular characterization of human Ro/SS-A antigen. Amino terminal sequence of
 A:Reference number: A28812; MUID:88273610; PMID:3260607
 A:Accession: A28812
 A:Molecule type: protein
 A:Residues: 18-41 <LIE>
 A>Note: 18-Ala was also found
 R:Dupuis, M.; Schaefer, E.; Krause, K.H.; Tschopp, J.
 J. Exp. Med. 177, 1-7, 1993
 A:Title: The calcium-binding protein calreticulin is a major constituent of lytic granul
 A:Reference number: PH1525; MUID:93115648; PMID:8418194
 A:Accession: PH1525

A:Molecule type: protein
 A:Residues: 18-27 <DUP>
 A:Experimental source: LAK cell
 R:Rojiani, M.V.; Finlay, B.B.; Gray, V.; Dedhar, S.
 Biochemistry 30, 9859-9866, 1991
 A:Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (calreticulin precursor) with a Ca(2+)-binding protein that co-purifies with the precursor
 A:Reference number: A40346; MUID:92002034; PMID:1911778
 A:Accession: A40346
 A:Molecule type: protein
 A:Residues: 18-34; R' <ROU>
 R:Krause, K.H.; Simmerman, H.K.B.; Jones, L.R.; Campbell, K.P.
 Biochem. J. 270, 545-548, 1990
 A:Title: Sequence similarity of calreticulin with a Ca(2+)-binding protein that co-purifies with the precursor
 A:Reference number: S11475; MUID:90380058; PMID:2400400
 A:Accession: S11475
 A:Molecule type: protein
 A:Residues: 18-32 <KRA>
 R:Damerdin, J.; McCreedy, P.; Stilwagen, S.; Ramirez, M.; Carrano, A.
 submitted to the EMBL Data Library, November 1996
 A:Description: Characterization by genomic sequence analysis of a gene-rich 111 kb region containing the calreticulin gene
 A:Reference number: Z22906
 A:Accession: T45075
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-417 <LAM>
 A:Cross-references: EMBL:AD000092; PIDN:AAB51176.1
 A:Experimental source: cell line SHL2-B; fibroblast
 C:Comment: Autoantibodies specific for this protein are found in Sjogren's syndrome and Sjogren's syndrome-like syndrome
 C:Genetics:
 A:Gene: GDB:CALR
 A:Cross-references: GDB:125179; OMIM:109091
 A:Map position: 19p13.3-19p13.2
 A:Introns: 31/1; 65/1; 133/1; 164/3; 234/3; 320/3; 351/3
 A>Note: CRT
 C:Superfamily: calreticulin
 C:Keywords: calcium binding; integrin binding
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:18-417/Product: calreticulin #status predicted <WAT>
 F:414-417/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 327; DB 1; Length 417;
 Best Local Similarity 100.0%; Pred. No. 1.4e-30;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVHVIFNYKGVNVLINKIRCKDDEFTHTLYTLVRPNTYEVKIDNSQVESGSL 60
 137 CGPGTKKVHVIFNYKGVNVLINKIRCKDDEFTHTLYTLVRPNTYEVKIDNSQVESGSL 196

Db 61 E 61
 197 E 197

RESULT 4
 A34154
 Calreticulin precursor, skeletal muscle - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A34154; S13047
 R:Fliegel, L.; Burns, K.; MacLennan, D.H.; Reithmeier, R.A.F.; Michalak, M.
 J. Biol. Chem. 264, 21522-21528, 1989
 A:Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin) cDNA from rabbit skeletal muscle
 A:Reference number: A34154; MUID:90094320; PMID:2600080
 A:Accession: A34154
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-418 <FLI>
 A:Cross-references: GB:J05138; NID:G164859; PIDN:AAA31188.1; PID:G164859
 R:Trevins, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meld
 Biochem. J. 271, 473-480, 1990
 A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage
 A:Reference number: S13045; MUID:910504414; PMID:2241926
 A:Accession: S13047

A:Molecule type: protein
 A:Residues: 19-32 <TRE>
 C:Superfamily: calreticulin
 C:Keywords: skeletal muscle
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:415-418/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 327; DB 1; Length 418;
 Best Local Similarity 100.0%; Pred. No. 1.4e-30;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVHVIFNYKGVNVLINKIRCKDDEFTHTLYTLVRPNTYEVKIDNSQVESGSL 60
 137 CGPGTKKVHVIFNYKGVNVLINKIRCKDDEFTHTLYTLVRPNTYEVKIDNSQVESGSL 196

Db 61 E 61
 197 E 197

RESULT 5
 S43376
 Calreticulin, brain isoform 1 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 20-Oct-1994 #sequence_revision 23-Mar-1995 #text_change 07-May-1999
 C:Accession: S43376; S36801
 R:Matsuoka, K.; Seta, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isobe, T.
 Biochem. J. 298, 435-442, 1994
 A:Title: Covalent structure of bovine brain calreticulin.
 A:Reference number: S43376; MUID:94183174; PMID:8135753
 A:Accession: S43376
 A:Molecule type: protein
 A:Residues: 1-400 <MAT>
 A:Experimental source: Brain
 R:Li, N.; Fine, R.E.; Johnson, R.J.
 Biochim. Biophys. Acta 1202, 70-76, 1993
 A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin
 A:Reference number: S36799; MUID:93385184; PMID:8373827
 A:Accession: S36801
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 45-63; E', 65-83 <LIU>
 A:Experimental source: Brain, clone 8.1
 C:Superfamily: calreticulin
 C:Keywords: calcium binding; glycoprotein
 F:397-400/Region: endoplasmic reticulum retention signal
 F:120-146/Dissulfide bonds: #status experimental
 F:162/Binding site: carbohydrate (Asn) #status experimental

Query Match 98.5%; Score 322; DB 2; Length 400;
 Best Local Similarity 98.4%; Pred. No. 5.3e-30;
 Matches 60; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVHVIFNYKGVNVLINKIRCKDDEFTHTLYTLVRPNTYEVKIDNSQVESGSL 60
 120 CGPGTKKVHVIFNYKGVNVLINKIRCKDDEFTHTLYTLVRPNTYEVKIDNSQVESGSL 179

Db 61 E 61
 180 E 180

RESULT 6
 S36799
 Calreticulin precursor, brain isoform 2 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 10-Dec-1993 #sequence_revision 23-Mar-1995 #text_change 13-Aug-1999
 C:Accession: S36799; S36800
 R:Li, N.; Fine, R.E.; Johnson, R.J.
 Biochim. Biophys. Acta 1202, 70-76, 1993
 A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin
 A:Reference number: S36799; MUID:93385184; PMID:8373827
 A:Accession: S36799

A:Molecule type: mRNA
 A:Residues: 1-421 <LIU>
 A:Cross-references: GB:L13462; NID:G948693; PIDN:AAC37307.1; PID:G348694
 A:Experimental source: brain, clone 9.4
 A:Accession: S36800
 A:Molecule type: protein
 A:Residues: 35-45 <L12>
 C:Superfamily: calreticulin
 C:Keywords: calcium binding; glycoprotein
 F:1-34/Domain: signal sequence #status predicted <SIG>
 F:35-42/Product: calreticulin, brain isoform 2 #status predicted <MAT>
 F:418-421/Region: endoplasmic reticulum retention signal
 F:141-167/Disulfide bonds: #status predicted
 F:183/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 98.5%; Score 322; DB 2; Length 421;
 Best Local Similarity 98.4%; Pred. No. 5.6e-30; Indels 0; Gaps 0;
 Matches 60; Conservative 1; Mismatches 0

QY 1 CGPGTKKVVHVFNYKGNVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 60
 DB 141 CGPGTKKVVHVFNYKGNVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 200

QY 61 E 61
 DB 201 E 201

RESULT 7
 JH0795
 calreticulin precursor - California sea hare
 N:Alternate names: protein 407
 C:Species: Aplysia californica (California sea hare)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 A:Accession: JH0795; B31409; F60977
 R:Kennedy, T.E.; Kuhl, D.; Barzilai, A.; Sweatt, J.D.; Kandel, E.R.
 Neuron 9, 1013-1024, 1992
 A:Title: Long-term sensitization training in aplysia leads to an increase in calreticulin
 A:Reference number: JH0795; MUID:93098937; PMID:1463604
 A:Accession: JH0795
 A:Molecule type: mRNA
 A:Residues: 1-405 <KEN>
 A:Cross-references: GB:S51239; NID:G262053; PIDN:AAB24569.1; PID:G262054
 A:Experimental source: abdominal ganglion and antral nervous system
 R:Kennedy, T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, E.R.; Sweatt, J.D.
 Proc. Natl. Acad. Sci. U.S.A. 85, 7008-7012, 1988
 A:Title: Sequencing of proteins from two-dimensional gels by using in situ digestion and
 tion in Aplysia.
 A:Reference number: A94207; MUID:88320566; PMID:3413132
 A:Accession: B31409
 A:Molecule type: protein
 A:Residues: 'X', 17-28, 'X', 30-31 <XE2>
 R:Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl, K.
 Electrophoresis 10, 152-157, 1989
 A:Title: Development of a database of amino acid sequences for proteins identified and i
 A:Reference number: A60977; MUID:89276264; PMID:2731514
 A:Accession: F60977
 A:Molecule type: protein
 A:Residues: 'X', 17-28, 'X', 30-31 <SWE>
 C:Superfamily: calreticulin
 C:Keywords: calcium binding; endoplasmic reticulum
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:16-405/Product: calreticulin #status predicted <MAT>
 F:402-405/Region: endoplasmic reticulum retention signal

Query Match 88.7%; Score 290; DB 1; Length 405;
 Best Local Similarity 85.2%; Pred. No. 3e-26; Indels 5; Gaps 0;
 Matches 52; Conservative 4; Mismatches 5

QY 1 CGPGTKKVVHVFNYKGNVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 60
 DB 133 CGPGTKKVVHVFNYKGNVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 192

QY 61 E 61
 DB 193 E 193

RESULT 8
 S29130
 calreticulin (clone 8) - African clawed frog (fragment)
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
 A:Accession: S29130; T01068
 R:Treves, S.; Zorzato, F.; Pozzan, T.
 Biochem. J. 287, 579-581, 1992
 A:Title: Identification of calreticulin isoforms in the central nervous system.
 A:Reference number: S29129; MUID:93074997; PMID:1445218
 A:Accession: S29130
 A:Molecule type: mRNA
 A:Residues: 1-384 <PRE>
 A:Cross-references: EMBL:X67598
 A:Accession: T01068
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-339, 'XTGR' <TRW>
 A:Cross-references: EMBL:X67598; NID:G64610; PIDN:CAA47867.1; PID:G64611
 A:Experimental source: CNS
 C:Superfamily: calreticulin
 C:Keywords: glycoprotein
 F:381-384/Region: endoplasmic reticulum retention signal
 F:316/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 87.8%; Score 287; DB 2; Length 384;
 Best Local Similarity 88.5%; Pred. No. 6.4e-26;
 Matches 54; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGPGTKKVVHVFNYKGNVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 60
 DB 109 CGPGTKKVVHVFNYKGNVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 168

QY 61 E 61
 DB 169 E 169

RESULT 9
 S29129
 calreticulin precursor (clone 3) - African clawed frog (fragment)
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
 A:Accession: S29129
 R:Treves, S.; Zorzato, F.; Pozzan, T.
 Biochem. J. 287, 579-581, 1992
 A:Title: Identification of calreticulin isoforms in the central nervous system.
 A:Reference number: S29129; MUID:93074997; PMID:1445218
 A:Accession: S29129
 A:Molecule type: mRNA
 A:Residues: 1-411 <TRW>
 A:Cross-references: EMBL:X67597; NID:G64608; PIDN:CAA47866.1; PID:G64609
 C:Superfamily: calreticulin
 C:Keywords: glycoprotein
 F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
 F:13-411/Product: calreticulin #status predicted <MAT>
 F:408-411/Region: endoplasmic reticulum retention signal
 F:339/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 87.8%; Score 287; DB 2; Length 411;
 Best Local Similarity 88.5%; Pred. No. 6.9e-26;
 Matches 54; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGPGTKKVVHVFNYKGNVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 60
 DB 132 CGPGTKKVVHVFNYKGNVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 191

QY 61 E 61

Db 192 E 192

RESULT 10
A56637
calreticulin homolog precursor - fruit fly (*Drosophila melanogaster*)
N:Alternate names: Ro/SS-A autoantigen/calreticulin homolog
C:Species: *Drosophila melanogaster*
C>Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 13-Aug-1999
C:Accession: A56637; A37158
R:Smith, M.J.
DNA Seq. 3, 247-250, 1992
A:Title: Nucleotide sequence of a *Drosophila melanogaster* gene encoding a calreticulin h
A:Reference number: A56637; MUID:93208374; PMID:1296819
A:Accession: A56637
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-406 <SMI>
A:Cross-references: GB:X64461; NID:97685; PIDN:CAA45791.1; PID:97686
A>Note: sequence extracted from NCBI backbone (NCBIN:128274, NCBIP:128275)
R:McCaulliffe, D.P.; Zappi, E.; Lieu, T.S.; Michalak, M.; Sontheimer, R.D.; Capra, J.D.
J. Clin. Invest. 86, 332-335, 1990
A:Title: A human Ro/SS-A autoantigen is the homologue of calreticulin and is highly hom
A:Reference number: A37158; MUID:9307981; PMID:2385822
A:Accession: A37158
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: DNA
A:Residues: 91-105, 'A', 107, 109-124, 182-183, 'L', 185-220 <MCC>
C:Genetics:
A:Gene: FlyBase: Crc
A:Cross-references: FlyBase: FBgn0005585
A:Introns: 65/1; 222/3
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-17/Domain: signal sequence #status predicted <SIG>
F:403-406/Region: endoplasmic reticulum retention signal

Query Match 85.0%; Score 278; DB 2; Length 406;
Best Local Similarity 83.6%; Pred. No. 7.7e-25;
Matches 51; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGPGTKKVHVIFNYKGNVLINCKDIRCKDDEFTHLYTLIVRPNTYEVKIDNSQVSGSL 60
137 CGPGTKKVHVIFSYKGNHLISKDIRCKDDVYTHLYTLIVRPNTYEVLDNEKVESGSL 196

Db 61 E 61
197 E 197

RESULT 11
S71343
calreticulin precursor - Korean frog
C:Species: *Rana rugosa* (Korean frog)
C>Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 20-Jun-2000
C:Accession: S71343
R:Yamamoto, S.; Nakamura, M.
FEBS Lett. 387, 27-32, 1996
A:Title: Calnexin: its molecular cloning and expression in the liver of the frog, *Rana*
A:Reference number: S71342; MUID:96234004; PMID:8654561
A:Accession: S71343
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-419 <YAM>
A:Cross-references: EMBL:D78589; NID:g1514956; PIDN:BAAL1425.1; PID:g1514957
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-419/Product: calreticulin #status predicted <YAT>
F:205-213/Region: nuclear location signal
F:415-418/Region: endoplasmic reticulum retention signal

Query Match 82.9%; Score 271; DB 2; Length 419;
Best Local Similarity 83.6%; Pred. No. 5.3e-24;
Matches 51; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGPGTKKVHVIFNYKGNVLINCKDIRCKDDEFTHLYTLIVRPNTYEVKIDNSQVSGSL 60
138 CGPGTKKVHVIFNYKGNVLINCKDIRSKADVSHLYTLIVRPNTYEVKIDNSQVSGSL 197

Db 61 E 61
198 E 198

RESULT 12
A32507
41K larval antigen - nematode (*Onchocerca volvulus*) (fragment)
C:Species: *Onchocerca volvulus*
C>Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 12-Apr-1995
C:Accession: A32507; A28813
J:Umasch, T.R.; Gallin, M.X.; Soboslay, P.T.; Erttmann, K.D.; Greene, B.M.
J. Clin. Invest. 82, 262-269, 1988
A:Title: Isolation and characterization of expression cDNA clones encoding antigens of
A:Reference number: A92769; MUID:98273584; PMID:2455736
A:Accession: A32507
A:Molecule type: mRNA
A:Residues: 1-336 <UNN>
C:Superfamily: calreticulin

Query Match 76.8%; Score 251; DB 2; Length 336;
Best Local Similarity 75.4%; Pred. No. 9.2e-22;
Matches 46; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 CGPGTKKVHVIFNYKGNVLINCKDIRCKDDEFTHLYTLIVRPNTYEVKIDNSQVSGSL 60
83 CGPGTKKVHVIFHYKDRNHMKDIRCKDDVTHLYTLIVNSDNTYEVQIDGKAESGEL 142

Db 61 E 61
143 E 143

RESULT 13
A48573
calreticulin autoantigen homolog precursor - fluke (*Schistosoma mansoni*)
C:Species: *Schistosoma mansoni*
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A48573
R:Khaliq, J.; Trottein, F.; Schacht, A.M.; Godin, C.; Pierce, R.J.; Capron, A.
Mol. Biochem. Parasitol. 57, 193-202, 1993
A:Title: Cloning of the gene encoding a *Schistosoma mansoni* antigen homologous to human
A:Reference number: A48573; MUID:93165070; PMID:8433712
A:Accession: A48573
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-393 <KHA>
A:Cross-references: GB:M93097; NID:g160928
A>Note: sequence inconsistent with the nucleotide translation
A>Note: sequence extracted from NCBI backbone (NCBIN:125085, NCBIP:125086)
C:Superfamily: calreticulin
F:1-16/Domain: signal sequence #status predicted <SIG>
F:390-393/Region: endoplasmic reticulum retention signal

Query Match 72.2%; Score 236; DB 1; Length 393;
Best Local Similarity 73.8%; Pred. No. 6.2e-20;
Matches 45; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CGPGTKKVHVIFNYKGNVLINCKDIRCKDDEFTHLYTLIVRPNTYEVKIDNSQVSGSL 60
135 CGMATKKVHVIFNYKGNHLIKKIPCKDDLKTHLYTLIVPNPNKYEVLDNAKVESGSL 194

Db 61 E 61
195 E 195

Db 143 CGYSTKKVHAI FNYNDTNHLIKDVPCEPDQLTHVTTILRPDATYSLIDNQBKQTGSL 202

Search completed: October 4, 2004, 13:06:34
Job time : 13.2765 secs

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RESULT 14
S25851
calreticulin precursor - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 06-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C:Accession: S25851; T33396
R:Smith, M.J.
DNA Seq. 2, 235-240, 1992
A:Title: A. C. elegans gene encodes a protein homologous to mammalian calreticulin.
A:Reference number: S25851; MUID:92329978; PMID:1627827
A:Accession: S25851
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-395 <SMI>
A:Cross-references: EMBL:X59589; NID:96693; PIDN:CAA42159.1; PID:96694
R:Bauer, C.; Courtney, L.; Lapiant, F.
submitted to the EMBL Data Library, February 1999
A:Description: The sequence of C. elegans cosmid Y38A10A.
A:Reference number: Z21453
A:Accession: T33996
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-395 <BAU>
A:Cross-references: EMBL:AF125963; PIDN:ADI4746.1; GSPDB:GNC0023; CESP:Y38A10A.5
A:Experimental source: Strain Bristol N2; Clone Y38A10A
C:Genetics:
A:Gene: CESP:Y38A10A.5
A:Map position: 5
A:Introns: 107/3; 315/3
C:Superfamily: calreticulin
F:1-15/Domain: signal sequence #status predicted <SIG>
F:392-395/Region: endoplasmic reticulum retention signal

Query Match 67.1%; Score 219.5; DB 2; Length 395;
Best Local Similarity 67.2%; Pred. No. 5.4e-18;
Matches 41; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

QY 1 CGPGTKVHVI FNYKGNVLNIDCKDDEPHLYTLVRPDNTVEVKIDNSQVESGSL 60
Db 133 CGP TRRVHVLN YAGENKLIKKEITCKSDHLYTLINSDNTVEVKIDGESAQIGSL 191

QY 61 E 61
Db 192 E 192

RESULT 15
Tl4554
calreticulin - beet
C:Species: Beta vulgaris (beet)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000
C:Accession: Tl4554
R:Viereck, R.
submitted to the EMBL Data Library, October 1997
A:Description: Nucleotide sequence from sugar beet calreticulin.
A:Reference number: Z18137
A:Accession: Tl4554
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-416 <VIE>
A:Cross-references: EMBL:AJ002057
A:Experimental source: strain diploide Inzuchtlinie KWS; leaf
C:Superfamily: calreticulin
C:Keywords: calcium binding

Query Match 59.0%; Score 193; DB 2; Length 416;
Best Local Similarity 56.7%; Pred. No. 7.3e-15;
Matches 34; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 1 CGPGTKVHVI FNYKGNVLNIDCKDDEPHLYTLVRPDNTVEVKIDNSQVESGSL 60
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2004, 12:52:12 ; Search time 8.97059 Seconds
(without alignments)
354.077 Million cell updates/sec

Title: US-09-807-148-5
Perfect score: 327
Sequence: 1 CGFGTKKHVIFNYKGNVL.....PNTYEVKIDNSQVSGSLE 61

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	327	100.0	416	1	CRTC_MOUSE
2	327	100.0	416	1	CRTC_MOUSE
3	327	100.0	417	1	CRTC_MOUSE
4	327	100.0	417	1	CRTC_MOUSE
5	327	100.0	418	1	CRTC_MOUSE
6	322	98.5	417	1	CRTC_MOUSE
7	322	98.5	421	1	CRTC_MOUSE
8	278	85.0	406	1	CRTC_MOUSE
9	251	76.8	388	1	CRTC_MOUSE
10	236	72.2	393	1	CRTC_MOUSE
11	219.5	67.1	395	1	CRTC_MOUSE
12	208	63.6	420	1	CRTC_MOUSE
13	193	59.0	416	1	CRTC_MOUSE
14	188	57.5	421	1	CRTC_MOUSE
15	186	56.9	415	1	CRTC_MOUSE
16	184	56.3	424	1	CRTC_MOUSE
17	182	55.7	380	1	CRTC_MOUSE
18	181	55.4	425	1	CRTC_MOUSE
19	181	55.4	424	1	CRTC_MOUSE
20	180	55.0	424	1	CRTC_MOUSE
21	178	54.4	416	1	CRTC_MOUSE
22	175	53.5	424	1	CRTC_MOUSE
23	170	52.0	420	1	CRTC_MOUSE
24	169.5	51.8	401	1	CRTC_MOUSE
25	163	49.8	416	1	CRTC_MOUSE
26	117.5	35.9	592	1	CALX_MOUSE
27	116.5	35.6	591	1	CALX_MOUSE
28	116.5	35.6	591	1	CALX_MOUSE
29	116.5	35.3	593	1	CALX_MOUSE
30	110.5	32.9	610	1	CALX_MOUSE
31	107.5	32.6	611	1	CALX_MOUSE
32	106.5	32.6	611	1	CALX_MOUSE
33	101.5	31.0	619	1	CALX_MOUSE

34	99	30.3	560	1	CALX_MOUSE
35	90.5	27.7	546	1	CALX_MOUSE
36	85.5	26.1	530	1	CALX_MOUSE
37	80.5	24.6	540	1	CALX_MOUSE
38	80.5	24.6	551	1	CALX_MOUSE
39	75.5	23.1	532	1	CALX_MOUSE
40	73.5	22.5	540	1	CALX_MOUSE
41	61.5	18.8	582	1	CALX_MOUSE
42	61	18.7	474	1	CALX_MOUSE
43	60.5	18.5	586	1	CALX_MOUSE
44	59.5	18.2	220	1	CALX_MOUSE
45	59.5	18.2	220	1	CALX_MOUSE

ALIGNMENTS

RESULT 1					
CRTC_MOUSE					
ID	CRTC_MOUSE	STANDARD	PRT	416 AA	
AC	P14211				
DT	01-JAN-1990 (Rel. 13, Created)				
DT	01-JAN-1990 (Rel. 13, Last sequence update)				
DT	15-MAR-2004 (Rel. 43, Last annotation update)				
DE	Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).				
GN	CALR.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.				
RP	STRAIN=BALB/C; TISSUE=Liver;				
RX	MEDLINE=90059955; PubMed=2583110;				
RA	Smith M.J., Koch G.L.E.;				
RT	Multiple zones in the sequence of calreticulin (CRP55, calregulin,				
RT	HACBP), a major calcium binding ER/SR protein.";				
RL	EMBO J. 8:3581-3586(1989).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=93013037; PubMed=1398135;				
RA	Mazzarella R.A., Gold P., Cunningham M., Green M.;				
RT	"determination of the sequence of an expressible cDNA clone encoding				
RT	Exp60/calregulin by the use of a novel nested set method.";				
RL	Gene 120:217-225(1992).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RP	STRAIN=FVB/N-3; TISSUE=Mammary gland;				
RX	MEDLINE=22398257; PubMed=12477932;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RA	Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,				
RA	Hopkins R.F., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Diatchenko L., Matovina K., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,				
RA	Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,				
RA	Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Vallalón D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,				
RA	Butterfield J.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,				
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;				
RT	"Generation and initial analysis of more than 15,000 full-length				
RT	human and mouse cDNA sequences.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
RN	[4]				
RP	SEQUENCE OF 18-38.				
RP	TISSUE=Fibroblast;				
RX	MEDLINE=95009907; PubMed=7523108;				

P36581	schizosacch
Q39817	glycine max
P29402	arabidopsis
Q39984	heliathus
Q82703	pisum sativ
Q38798	arabidopsis
P25201	acinetobact
Q32777	homo sapien
P48680	mus musculu
P21619	mus musculu
Q31537	rattus norv
P40555	saccharomyc

RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- FUNCTION: This protein binds calcium. There are both high and
CC low affinity calcium-binding sites.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: Belongs to the calreticulin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X14926; CAA33053.1; -;
DR EMBL; M92988; AAA37569.1; -;
DR EMBL; BC003453; AAH03453.1; -;
DR PIR; S06763; S06763;
DR SWISS-2DPAGE; P14211; MOUSE.
DR MGD; MGI:88252; Calr.
DR GO; GO:0005509; F:calcium ion binding; IDA.
DR InterPro; IPR009033; Calret calnex_P.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR008985; ConA-like lec_gl.
DR InterPro; IPR000886; ER target_S.
DR Pfam; PF00262; Calreticulin_1.
DR Pfam; PF00262; Calreticulin_1.
DR PRINTS; PIRSF02356; Calreticulin; 1.
DR PRINTS; PIRSF02356; Calreticulin.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN 1; 1.
DR PROSITE; PS00804; CALRETICULIN 2; 1.
DR PROSITE; PS00805; CALRETICULIN REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 416 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 416 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 202 221 1-2.
FT REPEAT 221 238 1-3.
FT REPEAT 238 255 1-4.
FT REPEAT 255 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 407 ASP/GLY/LYS-RICH.
FT DISULFID 127 163 BY SIMILARITY.
FT SITE 413 416 PREVENT SECRETION FROM ER.
SQ SEQUENCE 416 AA; 47994 MW; 24C03B00913408D8 CRC64;
Query Match 100.0%; Score 327; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.2e-32;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGPGTKKHVIFNYKGNVLINKIRCKDDEFTHTLYTLVIRPNTVEYKIDNSQVSGSL 60
Db 137 CGPGTKKHVIFNYKGNVLINKIRCKDDEFTHTLYTLVIRPNTVEYKIDNSQVSGSL 196
QY 61 E'61
Db 197 E 197
RESULT 2
CRIC_RAT STANDARD; PR7; 416 AA.
ID CRIC_RAT

AC P18418; P10452;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (BRP60) (CALBP)
DE (Calcium-binding protein 3) (CABP3).
GN CALR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=brain cortex;
RX MEDLINE=90370496; PubMed=2395661;
RA Murthy K.K., Banville D., Srikanth C.B., Carrier F., Bell A.,
RA Holmes C., Patel Y.C.;
RA "Structural homology between the rat calreticulin gene product and
RT the Onchocerca volvulus antigen Ral-1.";
RL Nucleic Acids Res. 18:4933-4933(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=93202172; PubMed=8453984;
RA Nakamura M., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai K.,
RA Okinaga S., Kobayashi T.;
RA "An endoplasmic reticulum protein, calreticulin, is transported into
RT the acrosome of rat sperm.";
RL Exp. Cell Res. 205:101-110(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=liver;
RX MEDLINE=95181573; PubMed=7876339;
RA Soennichsen B., Fuellekrug J., van Nguyen P., Diekmann W.,
RA Robinson D.G., Mieskes G.;
RA "Retention and retrieval: both mechanisms cooperate to maintain
RT calreticulin in the endoplasmic reticulum.";
RL J. Cell Sci. 107:2705-2717(1994).
RN [4]
RP SEQUENCE OF 270-358 FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Lone Y.C., Bailly A., Latruffe N.;
RL Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 18-29.
RX MEDLINE=91054414; PubMed=2241926;
RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
RA Maciennan D.H., Meldolesi J., Pozzan T.;
RA "Calreticulin is a candidate for a calsequestrin-like function in
RT Ca2(+)-storage compartments (calciosomes) of liver and brain.";
RL Biochem. J. 271:473-480(1990).
RN [6]
RP SEQUENCE OF 18-32.
RC STRAIN=Sprague-Dawley; TISSUE=testis;
RX MEDLINE=92360010; PubMed=1497655;
RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;
RA "Calreticulin is present in the acrosome of spermatids of rat
RT testis.";
RL Biochem. Biophys. Res. Commun. 186:668-673(1992).
RN [7]
RP SEQUENCE OF 18-32.
RC STRAIN=LEC; TISSUE=Liver;
RX MEDLINE=94072621; PubMed=8251535;
RA Yokoi T., Nagayama S., Kajiura R., Kawaguchi Y., Horiuchi R.,
RA Kamataki T.;
RA "Identification of protein disulfide isomerase and calreticulin as
RT autoantigenic antigens in LEC strain of rats.";
RL Biochim. Biophys. Acta 1158:339-344(1993).
CC -!- FUNCTION: This protein binds calcium. There are both high and low
CC affinity calcium-binding sites.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: Belongs to the calreticulin family.

CC -!- CAUTION: Was originally (Ref.2) thought to be D-beta-
CC hydroxybutyrate dehydrogenase.
CC -----
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CC -----

CC EMBL; D78308; BAA11345.1; -
CC EMBL; X53363; CAA37446.1; -
CC EMBL; X13702; CAA31987.1; ALT_SEQ.
CC EMBL; X79327; CAA5890.1; -
CC PIR; JH0819; JH0819.
CC PDB; 1HHN; 26-FEB-02.
CC PDB; 1K91; 12-OCT-02.
CC PDB; 1K9C; 12-OCT-02.
CC InterPro; IPR009033; Calret calnex_P.
CC InterPro; IPR001580; Calreticulin.
CC InterPro; IPR008985; ConA_like lec_gl.
CC InterPro; IPR000866; ER_target_S.
CC Pfam; PF00262; calreticulin; 1.
CC PRINTS; P00626; Calreticulin; 1.
CC PROSITE; PS00014; ER_TARGET; 1.
CC PROSITE; PS00803; CALRETICULIN_1; 1.
CC PROSITE; PS00804; CALRETICULIN_2; 1.
CC PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
CC KEGG; Endoplasmic reticulum; Calcium-binding; Repeat; Signal; 3D-structure.
CC FT SIGNAL 1 17
CC FT CHAIN 18 416 CALRETICULIN.
CC FT DOMAIN 18 197 N-DOMAIN.
CC FT DOMAIN 198 308 P-DOMAIN.
CC FT DOMAIN 309 416 C-DOMAIN.
CC FT REPEAT 191 255 4 X APPROXIMATE REPEATS.
CC FT REPEAT 210 221 1-1.
CC FT REPEAT 227 238 1-2.
CC FT REPEAT 244 255 1-3.
CC FT REPEAT 259 269 1-4.
CC FT REPEAT 273 283 2-1.
CC FT REPEAT 287 297 2-2.
CC FT REPEAT 351 407 ASP/GLU/LYS-RICH.
CC FT DISULFID 137 163 BY SIMILARITY.
CC FT SITE 413 416 PREVENT SECRETION FROM ER.
CC FT SITE 416 416 PREVENT SECRETION FROM ER.
CC SQ SEQUENCE 416 AA; 47995 MW; 286713CED31A2970 CRC64;

Query Match 100.0%; Score 327; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.2e-32;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINCKDKDEFTHTLYTLVIRPDNTYEVKIDNSQVESGSL 60
DB 137 CGPGTKKHVIFNYKGNVLINCKDKDEFTHTLYTLVIRPDNTYEVKIDNSQVESGSL 196
QY 61 E 61
DB 197 E 197

RESULT 3
ID -CRTC CRIGR STANDARD; PRT; 417 AA.
AC Q8K3H7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERp60).
GN CALR.

OS Cricetus griseus (Chinese hamster).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
CC Cricetus.
CC NCBI_TaxID=10029;
CC [1]
CC SEQUENCE FROM N.A.
CC Chung J.Y., Lee G.M.;
CC Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: This protein binds calcium. There are both high and low
CC affinity calcium-binding sites.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: Belongs to the calreticulin family.
CC -----
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CC -----

CC EMBL; AY100688; AAM48568.1; -
CC InterPro; IPR009033; Calret calnex_P.
CC InterPro; IPR001580; Calreticulin.
CC InterPro; IPR008985; ConA_like lec_gl.
CC InterPro; IPR000866; ER_target_S.
CC Pfam; PF00262; calreticulin; 1.
CC PIRSF; PIRSF002356; Calreticulin; 1.
CC PRINTS; P00626; Calreticulin.
CC PRODOM; P000866; Calreticulin; 1.
CC PROSITE; PS00803; CALRETICULIN_1; 1.
CC PROSITE; PS00804; CALRETICULIN_2; 1.
CC PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
CC PROSITE; PS00014; ER_TARGET; 1.
CC KEGG; Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein; Signal.
CC FT SIGNAL 1 17 BY SIMILARITY.
CC FT CHAIN 18 417 CALRETICULIN.
CC FT DOMAIN 18 197 N-DOMAIN.
CC FT DOMAIN 198 308 P-DOMAIN.
CC FT DOMAIN 309 417 C-DOMAIN.
CC FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
CC FT REPEAT 191 202 1-1.
CC FT REPEAT 210 221 1-2.
CC FT REPEAT 227 238 1-3.
CC FT REPEAT 244 255 1-4.
CC FT REPEAT 259 297 2-1.
CC FT REPEAT 273 283 2-2.
CC FT REPEAT 287 297 2-3.
CC FT REPEAT 351 407 ASP/GLU/LYS-RICH.
CC FT DISULFID 137 163 BY SIMILARITY.
CC FT SITE 414 417 PREVENT SECRETION FROM ER (POTENTIAL).
CC SQ SEQUENCE 417 AA; 48242 MW; D617DA37D14F2D45 CRC64;

Query Match 100.0%; Score 327; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.2e-32;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINCKDKDEFTHTLYTLVIRPDNTYEVKIDNSQVESGSL 60
DB 137 CGPGTKKHVIFNYKGNVLINCKDKDEFTHTLYTLVIRPDNTYEVKIDNSQVESGSL 196
QY 61 E 61
DB 197 E 197

RESULT 4
ID -CRTC HUMAN STANDARD; PRT; 417 AA.
AC P27797;

DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).
 GN CALR OR CRTG.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92013129; PubMed=1919005;
 RA Rokeach L.A., Haselby J.A., Meilof J.F., Smeenk R.J., Unnasch T.R.,
 RA Greene B.M., Hoch S.O.;
 RA "Characterization of the autoantigen calreticulin.";
 RL J. Immunol. 147:3031-3039 (1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90237213; PubMed=2332496;
 RA McCaulliffe D.P., Lux F.A., Lieu T.S., Sanz I., Hanke J., Newkirk M.M.,
 RA Bachinski L.L., Itch Y., Siciliano M.J., Reichlin M., Sontheimer R.D.,
 RA Capra J.D.;
 RA "Molecular cloning, expression, and chromosome 19 localization of a
 human Ro(SS-A) autoantigen.";
 RL J. Clin. Invest. 85:1379-1391 (1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92129342; PubMed=1733953;
 RA McCaulliffe D.P., Yang Y.S., Wilson J., Sontheimer R.D., Capra J.D.;
 RA "The 5'-flanking region of the human calreticulin gene shares
 RT homology with the human GRP78, GRP94, and protein disulfide isomerase
 RT promoters.";
 RL J. Biol. Chem. 267:2557-2562 (1992).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92129342; PubMed=1733953;
 RA Liu J., Peng X., Yuan J., Qiang B.;
 RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX Lamerdin J.E., McCreedy P.M., Stilwagen S., Ramirez M., Carrano A.;
 RA "Characterization by genomic sequence analysis of a gene-rich 111 kb
 RT region of 19p13.2 containing the human DNA repair gene, RAD23A.";
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Eye, Pancreas, and Skin;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeng B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
 RN [7]
 RP SEQUENCE OF 18-36.
 RX MEDLINE=9202034; PubMed=1911778;
 RA Rojiani M.V., Finlay B.B., Gray V., Dedhar S.;
 RA "In vitro interaction of a polypeptide homologous to human Ro(SS-A
 RT antigen (calreticulin) with a highly conserved amino acid sequence in

the cytoplasmic domain of integrin alpha subunits.";
 RL Biochemistry 30:9859-9866 (1991).
 RN [8]
 RP SEQUENCE OF 18-32.
 RX MEDLINE=90380058; PubMed=2400400;
 RA Krause K.H., Simerman H.K., Jones L.R., Campbell K.P.;
 RA "Sequence similarity of calreticulin with a Ca2(+)-binding protein
 RT that co-purifies with an Ins(1,4,5)P3-sensitive Ca2+ store in HL-60
 RT cells.";
 RL Biochem. J. 270:545-548 (1990).
 RN [9]
 RP SEQUENCE OF 18-28.
 RX TISSUE=Liver;
 RA MEDLINE=93162045; PubMed=1286669;
 RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
 RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargha R.,
 RA Appel R.D., Hughes G.J.;
 RA "Human liver protein map: a reference database established by
 RT microsequencing and gel comparison.";
 RL Electrophoresis 13:992-1001 (1992).
 RN [10]
 RP PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.
 RX TISSUE=Keratinocytes;
 RA MEDLINE=93162043; PubMed=1286667;
 RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
 RA Vandekerckhove J.;
 RA "Microsequences of 145 proteins recorded in the two-dimensional gel
 RT protein database of normal human epidermal keratinocytes.";
 RL Electrophoresis 13:960-969 (1992).
 RN [11]
 RP SEQUENCE OF 18-26.
 RX TISSUE=Colon carcinoma;
 RA MEDLINE=97295306; PubMed=9150948;
 RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
 RA "A two-dimensional gel database of human colon carcinoma proteins.";
 RL Electrophoresis 18:605-613 (1997).
 CC -!- FUNCTION: This protein binds calcium. There are both high and low
 CC affinity calcium-binding sites.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -!- SIMILARITY: Belongs to the calreticulin family.
 CC -!- CAUTION: Was originally (Ref.2) thought to be the 52 kDa Ro
 CC autoantigen.
 CC
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 CC
 CC EMBL; M84739; AAA51916.1; -;
 CC EMBL; M32294; AAA36582.1; -;
 CC EMBL; AY047586; AAL1126.1; -;
 CC EMBL; AD000092; AAB51176.1; -;
 CC EMBL; BC002500; AA02500.1; -;
 CC EMBL; BC007911; AA07911.1; -;
 CC EMBL; BC020493; AA020493.1; -;
 CC PIR; A42330; A37047.
 CC PDB; 2CLR; 31-MAR-95.
 CC SWISS-2DPAGE; P27797; HUMAN
 CC Aarhuus/Ghent-2DPAGE; 9401; IEP.
 CC HSC-2DPAGE; P27797; HUMAN.
 CC PHCI-2DPAGE; P27797; -;
 CC SIENA-2DPAGE; P27797; -;
 CC SIENA-2DPAGE; P27797; -;
 CC Genew; HGNC:1455; CALR.
 CC MIM; 109091; -;
 CC GO; GO:006355; P-regulation of transcription, DNA-dependent; TAS.
 CC InterPro; IPR009033; Calret_calmex_P.
 CC InterPro; IPR001580; Calreticulin.
 CC InterPro; IPR008985; ConA_like lec_gl.

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DR InterPro; IPR000886; ER_target_S.
DR Pfam; PF00262; calreticulin; 1.
DR PIRSF; PIRSF002356; Calreticulin; 1.
DR PRINTS; PRO0626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; 3D-structure.
FT SIGNAL 1 17
FT CHAIN 18 417 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 417 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT REPEAT 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 269 297 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 414 417 PREVENT SECRETION FROM ER.
FT CONFLICT 35 35 MISSING (IN REF. 3)
SQ SEQUENCE 417 AA; 48141 MW; BC37C3C0F1034F82 CRC64;

Query Match 100.0%; Score 327; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.2e-32;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVVHFNFKGNVLNKIRCKDDEFTHTLYLIVRPDNTYEVKIDNSQVSGSL 60
Db 137 CGPGTKKVVHFNFKGNVLNKIRCKDDEFTHTLYLIVRPDNTYEVKIDNSQVSGSL 196

QY 61 E 61
Db 197 E 197

RESULT 5
CRTC_RABIT
ID CRTC_RABIT STANDARD; PRT; 418 AA.
AC P15253;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).
GN CALR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=slow-twitch skeletal muscle;
RX MEDLINE=90094320; PubMed=2600080;
RA Fliegel L., Burns K., MacLennan D.H., Reithmeier R.A.F., Michalak M.;
RT "Molecular cloning of the high affinity calcium-binding protein
(calsequestrin) of skeletal muscle sarcoplasmic reticulum.";
RL J. Biol. Chem. 264:21522-21528 (1989).
RN [2]
RN SEQUENCE FROM N.A.
RC TISSUE=Fast-twitch skeletal muscle;
RX MEDLINE=91282795; PubMed=2059224;
RA Fliegel L., Michalak M.;
RT "Fast-twitch and slow-twitch skeletal muscles express the same
isoform of calreticulin.";
RL Biochem. Biophys. Res. Commun. 177:979-984 (1991).
RN [3]

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RP SEQUENCE OF 18-36.
RX MEDLINE=91054414; PubMed=2241926;
RA Treves S., de Mattei M., Lanfretti M., Villa A., Green N.M.,
RA MacLennan D.H., Meldolesi J., Pozzan T.;
RT "Calreticulin is a candidate for a calsequestrin-like function in
Ca2(+)-storage compartments (calciosomes) of liver and brain.";
RL Biochem. J. 271:473-480 (1990).
RN [4]
RP SEQUENCE OF 18-46.
RX MEDLINE=91201375; PubMed=2016321;
RA Milner R.E., Bakesh S., Shemanko C., Carpenter M.R., Smillie L.,
RA Vance J.E., Opas M., Michalak M.;
RT "Calreticulin, and not calsequestrin, is the major calcium binding
protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic
reticulum.";
RL J. Biol. Chem. 266:7155-7165 (1991).
RN [5]
RP PARTIAL SEQUENCE.
RX TISSUE=Lung;
RX MEDLINE=92002038; PubMed=1911780;
RA Guan S., Falick A.M., Williams D.E., Cashman J.R.;
RT "Evidence for complex formation between rabbit lung flavin-containing
monooxygenase and calreticulin.";
RL Biochemistry 30:9892-9900 (1991).
CC -!- FUNCTION: This protein binds calcium. There are both high and low
affinity calcium-binding sites.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: Belongs to the calreticulin family.
CC
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CC
CC EMBL; J05138; AAA31188.1; -.
DR PIR; A34154; A34154.
DR PIR; C33208; C33208.
DR PIR; S13046; S13046.
DR InterPro; IPR009033; Calret calnex_P.
DR InterPro; IPR001580; Calreticulin_P.
DR InterPro; IPR008985; ConA_like_rec_gl.
DR InterPro; IPR000886; ER_target_S.
DR Pfam; PF00262; calreticulin; 1.
DR PIRSF; PIRSF002356; Calreticulin; 1.
DR PRINTS; PRO0626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 418 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 418 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT REPEAT 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 269 297 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 415 418 PREVENT SECRETION FROM ER.
FT VARIANT 35 35 E -> D.

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FT  CONFLICT  90      90      P -> T (IN REF. 5).
SQ  SEQUENCE  418 AA;  48275 MW;  B6082B689DC763A6 CRC64;

Query Match      100.0%; Score 327; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 1.2e-32;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 CGPGTKKHVIFNYKGNVLINKDIRKDEFFHLYTLIVRPNTYEVKIDNSQVESGSL 60
    |||
Db  137 CGPGTKKHVIFNYKGNVLINKDIRKDEFFHLYTLIVRPNTYEVKIDNSQVESGSL 196
    |||

Qy  61 E 61
    |
Db  197 E 197

RESULT 6
CRT1_BOVIN STANDARD; PRT; 417 AA.
ID CRT1_BOVIN STANDARD; PRT; 417 AA.
AC P21239; Q8S053;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Calreticulin, brain isoform 1 precursor (CRP55) (Calregulin) (HACBP).
GN CALR OR CRT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Hossain M.A., Takawa K., Minakata H., Nakajima T.;
RT "Bovine brain calreticulin."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 18-417.
RC TISSUE=Brain;
RA Matsuoka K., Seta K., Yamakawa Y., Okuyama T., Shinoda T., Isobe T.;
RT "Covalent structure of bovine brain calreticulin."
RL Biochem. J. 298:435-442(1994).
CC -!- FUNCTION: This protein binds calcium. There are both high and low
CC affinity calcium-binding sites.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: Belongs to the calreticulin family.
CC
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CC -----
CC EMBL; AB067687; BAB86913.1;
CC InterPro; IPR009033; Calret calnex_P.
CC InterPro; IPR001580; Calreticulin.
CC InterPro; IPR008985; ConA_likelec-gl.
CC Pfam; PF00262; calreticulin; 1.
CC PRINTS; PRS002356; Calreticulin.
CC ProDom; PD01866; Calreticulin; 1.
CC PROSITE; PS00014; ER TARGET; 1.
CC PROSITE; PS00803; CALRETICULIN_1; 1.
CC PROSITE; PS00804; CALRETICULIN_2; 1.
CC PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
CC Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein; Signal.
FT SIGNAL 1 17
CHAIN 18 417 CALRETICULIN, BRAIN ISOFORM 1.

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FT  DOMAIN  18      197      N-DOMAIN.
FT  DOMAIN  198      308      P-DOMAIN.
FT  DOMAIN  309      417      C-DOMAIN.
FT  REPEAT  191      255      4 X APPROXIMATE REPEATS.
FT  REPEAT  210      221      1-1.
FT  REPEAT  227      238      1-2.
FT  REPEAT  244      255      1-3.
FT  REPEAT  259      297      1-4.
FT  REPEAT  269      297      3 X APPROXIMATE REPEATS.
FT  REPEAT  273      283      2-1.
FT  REPEAT  287      297      2-2.
FT  REPEAT  297      307      2-3.
FT  DOMAIN  351      407      ASP/GLU/LYS-RICH.
FT  DISULFID 137      163      N-LINKED (GLCNAC. .).
FT  CARBOHYD 179      179      PREVENT SECRETION FROM ER (POTENTIAL).
FT  SITE  414      417      PREVENT SECRETION FROM ER (POTENTIAL).
SQ  SEQUENCE  417 AA;  48038 MW;  7BF812C7B5417BE9 CRC64;

Query Match      98.5%; Score 322; DB 1; Length 417;
Best Local Similarity 98.4%; Pred. No. 4.9e-32;
Matches 60; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  1 CGPGTKKHVIFNYKGNVLINKDIRKDEFFHLYTLIVRPNTYEVKIDNSQVESGSL 60
    |||
Db  137 CGPGTKKHVIFNYKGNVLINKDIRKDEFFHLYTLIVRPNTYEVKIDNSQVESGSL 196
    |||

Qy  61 E 61
    |
Db  197 E 197

RESULT 7
CRT2_BOVIN STANDARD; PRT; 421 AA.
ID CRT2_BOVIN STANDARD; PRT; 421 AA.
AC P42918;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Calreticulin, brain isoform 2 precursor (CRP55) (Calregulin) (HACBP).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93385184; PubMed=8373827;
RA Liu N., Fine R.E., Johnson R.J.;
RT "Comparison of cDNAs from bovine brain coding for two isoforms of
RT calreticulin."
RL Biochim. Biophys. Acta 1202:70-76(1993).
CC -!- FUNCTION: This protein binds calcium. There are both high and low
CC affinity calcium-binding sites.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: Belongs to the calreticulin family.
CC
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CC -----
CC EMBL; L13462; AAC37307.1;
CC PIR; S36799; S36799.
CC InterPro; IPR009033; Calret calnex_P.
CC InterPro; IPR001580; Calreticulin.
CC InterPro; IPR008985; ConA_likelec-gl.
CC InterPro; IPR00886; ER target_S.
CC Pfam; PF00262; calreticulin; 1.

```

DR PIRSF; PIRSF002356; Calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN 1; 1.
DR PROSITE; PS00804; CALRETICULIN 2; 1.
DR PROSITE; PS00805; CALRETICULIN REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 34
FT CHAIN 35 421
FT DOMAIN 35 201 N-DOMAIN.
FT DOMAIN 202 312 P-DOMAIN.
FT DOMAIN 313 421 C-DOMAIN.
FT DOMAIN 195 259 4 X APPROXIMATE REPEATS.
FT REPEAT 195 206 1-1.
FT REPEAT 214 225 1-2.
FT REPEAT 231 242 1-3.
FT REPEAT 248 259 1-4.
FT REPEAT 263 301 3 X APPROXIMATE REPEATS.
FT REPEAT 263 273 2-1.
FT REPEAT 277 287 2-2.
FT REPEAT 291 301 2-3.
FT DOMAIN 366 411 ASP/GLU/LYS-RICH.
FT DISULFID 141 167 BY SIMILARITY.
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 418 421 PREVENT SECRETION FROM ER.
SQ SEQUENCE 421 AA; 48812 MW; 0257E959F71528BC CRC64;

Query March 98.5%; Score 322; DB 1; Length 421;
Best Local Similarity 98.4%; Pred. No. 4.9e-32;
Matches 60; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGPCTKKVHVFYFKGNVLINLKIRCKDDEFTHTLYTLVIRPNTYEVKIDNSQVSGSL 60
Db 141 CGPCTKKVHVFYFKGNVLINLKIRCKDDEFTHTLYTLVIRPNTYEVKIDNSQVSGSL 200

Qy 61 E 61
Db 201 E 201

RESULT 8
ID CRTIC DROME STANDARD; PRT; 406 AA.
AC P29413; Q9VHA3;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP).
GN CRC OR CG9429.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93208374; PubMed=1296819;
RA Smith M.J.;
RT "Nucleotide sequence of a Drosophila melanogaster gene encoding a
RL calreticulin homologue.";
RL DNA Seq. 3:247-250(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Bfannkoch C., Baldwin D.,

RA Balaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Danke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleschmann W.,
RA Foslter A., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwa C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Massarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [3]
RP SEQUENCE OF 91-124 AND 182-220.
RX MEDLINE=90307981; PubMed=2365822;
RA McCaulliffe D.F., Zappi E., Lieu T.S., Michalak M., Sontheimer R.D.,
RA Capra J.D.;
RT "A human Ro/SS-A autoantigen is the homologue of calreticulin and is
RT highly homologous with onchocercal RAL-1 antigen and an aplysia
RT memory molecule.";
RL J. Clin. Invest. 86:332-335(1990).
CC -!- FUNCTION: This protein binds calcium. There are both high and low
CC affinity calcium-binding sites.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: Belongs to the calreticulin family.
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CC -----
CC EMBL; X64461; CAA45791.1; -;
CC EMBL; AE003683; AAF54416.1; -;
CC PIR; A56637; A56637.
CC FlyBase; FBgn0005585; Crc.
CC GO; GO:0007417; P:central nervous system development; IMP.
CC InterPro; IPR009033; Calret calnex_P.
CC InterPro; IPR001580; Calreticulin.
CC InterPro; IPR008985; ConA_like_rec_gl.
CC InterPro; IPR000886; ER target_S.
CC Pfam; PF00262; calreticulin; 1.
CC PIRSF; PIRSF02356; Calreticulin; 1.
CC PRINTS; PR00626; CALRETICULIN.
CC PRODOM; PD001866; Calreticulin; 1.
CC PROSITE; PS00014; ER_TARGET; 1.
CC PROSITE; PS00803; CALRETICULIN 1; 1.
CC PROSITE; PS00804; CALRETICULIN 2; 1.
CC PROSITE; PS00805; CALRETICULIN REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 406 CALRETICULIN.

FT CONFLICT 107 107 G -> A (IN REF. 3).
 FT CONFLICT 184 184 V -> L (IN REF. 3).
 SQ SEQUENCE 406 AA; 46808 MW; 65D72C69D0BEC427 CRC64;
 Query Match 85.0%; Score 278; DB 1; Length 406;
 Best Local Similarity 83.6%; Pred. No. 1.2e-26;
 Matches 51; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CGPGTKVHVIFNYKGNVLNKKDKDEFFHLYTLIVRPNTYEVKIDNSQVSGSL 60
 DB 137 CGPGTKVHVIFSYKGNHLSKDKCKDDVYTHFYTLIVRPNTYEVKIDNEKVSGL 196
 QY 61 E 61
 DB 197 E 197
 RESULT 9
 RALI_ONCVO STANDARD; PRT; 388 AA.
 AC P11012;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE RAL-1 protein precursor (41 kDa larval antigen).
 GN RALI.
 OS Onchocerca volvulus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 OC Onchocercidae; Onchocerca.
 OX NCBI_TaxID=6282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94341871; PubMed=7520419;
 RA Rokeach L.A., Zimmerman P.A., Unnasch T.R.;
 RT "Epitopes of the Onchocerca volvulus RALI antigen, a member of the
 RT calreticulin family of proteins, recognized by sera from patients
 RT with onchocerciasis";
 RL Infect. Immun. 62:3696-3704 (1994).
 RN [2]
 RP SEQUENCE OF 53-388 FROM N.A.
 RX MEDLINE=88273584; PubMed=2455736;
 RA Unnasch T.R., Gallin M.Y., Soboslay P.T., Ettmann K.D., Greene B.M.;
 RT "Isolation and characterization of expression cDNA clones encoding
 RT antigens of Onchocerca volvulus infective larvae";
 RL J. Clin. Invest. 92:262-269 (1998).
 CC -1- SIMILARITY: Belongs to the calreticulin family.
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 CC -----
 CC EMBL; M20565; AAA59056.1; -
 CC PIR; A32507; A32507.
 CC InterPro; IPR009033; Calret. calnex P.
 CC InterPro; IPR001580; Calreticulin.
 CC InterPro; IPR008985; ConAlike Lec. gl.
 CC Pfam; PF00262; calreticulin; 1.
 CC PRINTS; PIRSF002356; Calreticulin; 1.
 CC PROSITE; PS00626; CALRETICULIN.
 CC ProDom; PD001866; Calreticulin; 1.
 CC PROSITE; PS00803; CALRETICULIN; 1.
 CC PROSITE; PS00804; CALRETICULIN; 2; 1.
 CC PROSITE; PS00805; CALRETICULIN REPEAT; 3.
 CC Calcium-binding; Repeat; Antigen; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 388
 FT DOMAIN 189 253 4 X APPROXIMATE REPEATS.
 FT REPEAT 189 200 1-1.
 FT REPEAT 206 219 1-2.

FT REPEAT 225 236 1-3.
 FT REPEAT 242 253 1-4.
 FT DOMAIN 257 295 3 X APPROXIMATE REPEATS.
 FT REPEAT 257 267 2-1.
 FT REPEAT 271 281 2-2.
 FT REPEAT 285 295 2-3.
 FT DOMAIN 353 388 ARG/LYS-RICH (BASIC).
 FT DISULFID 135 161 BY SIMILARITY.
 SQ SEQUENCE 388 AA; 45298 MW; 9537F298A2D31CD6 CRC64;
 Query Match 76.8%; Score 251; DB 1; Length 388;
 Best Local Similarity 75.4%; Pred. No. 2.4e-23;
 Matches 46; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
 QY 1 CGPGTKVHVIFNYKGNVLNKKDKDEFFHLYTLIVRPNTYEVKIDNSQVSGSL 60
 DB 135 CGPGTKVHVIFHYKDRNMIKKDKDDVFTHLYTLIVNSDNTYEVQIDGKESGEL 194
 QY 61 E 61
 DB 195 E 195
 RESULT 10
 CRIC_SCHMA STANDARD; PRT; 393 AA.
 AC Q06814; Q26562;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Calreticulin precursor (SM4 protein).
 OS Schistosoma mansoni (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
 OC Schistosomatoidea; Schistosomatidae; Schistosoma.
 OX NCBI_TaxID=6183;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Puerto Rican;
 RC MEDLINE=93165070; PubMed=8433712;
 RA Khalife J., Trottein F., Schacht A.-M., Godin C., Pierce R.J.,
 RA Capron A.;
 RT "Cloning of the gene encoding a Schistosoma mansoni antigen
 RT homologous to human Ro/SS-A autoantigen";
 RL Mol. Biochem. Parasitol. 57:193-202 (1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Puerto Rican;
 RC MEDLINE=94187805; PubMed=8139623;
 RA Khalife J., Pierce R.J., Godin C., Capron A.;
 RT "Cloning and sequencing of the gene encoding Schistosoma mansoni
 RT calreticulin";
 RL Mol. Biochem. Parasitol. 62:313-315 (1993).
 CC -1- FUNCTION: This protein binds calcium. There are both high and low
 CC affinity calcium-binding sites.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: Belongs to the calreticulin family.
 CC -----
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 CC -----
 CC EMBL; M93037; AAA29854.1; -
 CC EMBL; L24159; AAA19024.1; -
 CC InterPro; IPR009033; Calret. calnex P.
 CC InterPro; IPR001580; Calreticulin.
 CC InterPro; IPR008985; ConAlike Lec. gl.
 CC InterPro; IPR008866; ER_target_S.
 CC Pfam; PF00262; calreticulin; 1.
 CC PRINTS; PIRSF002356; Calreticulin; 1.
 CC PIRSF; PIRSF002356; Calreticulin; 1.

PRINTS; PRO0626; CALRETICULIN.
 ProDom: PD001866; Calreticulin; 1.
 PROSITE; PS00014; ER TARGET; 1.
 PROSITE; PS00803; CALRETICULIN_1; 1.
 PROSITE; PS00803; CALRETICULIN_2; 1.
 PROSITE; PS00804; CALRETICULIN_REPEAT; 1.
 PROSITE; PS00805; CALRETICULIN_REPEAT; 1.
 Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
 SIGNAL 1 16
 CHAIN 17 393
 DOMAIN 189 254
 REPEAT 189 254
 REPEAT 189 254
 REPEAT 209 220
 REPEAT 209 220
 REPEAT 225 236
 REPEAT 243 254
 REPEAT 257 295
 REPEAT 257 295
 REPEAT 271 281
 REPEAT 271 281
 REPEAT 285 295
 REPEAT 285 295
 CARBOHYD 27 27
 DISULFID 135 161
 SITE 390 393
 SITE 390 393
 CONFLICT 89 90
 CONFLICT 188 207
 CONFLICT 188 207
 CONFLICT 378 393
 SEQUENCE 393 AA; 45397 MW; 45F59857C21940D2 CRC64;
 Query Match 72.2%; Score 236; DB 1; Length 393;
 Best Local Similarity 73.8%; Pred. No. 1.7e-21;
 Matches 45; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 QY 1 CGPGTKKHVTFNFKGKVNLIKIRCKDDFTHLVTPDNTVEVKIDNSQVESGSL 60
 135 COMATKKVHVTFNFKGKVNLIKIRCKDDFTHLVTPDNTVEVKIDNSQVESGSL 194
 61 E 61
 195 E 195
 RESULT 11
 ID CRTCC CAEEL STANDARD; PRT; 395 AA.
 AC P27798;
 ID 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Calreticulin precursor.
 CRT-1 OR Y38A10A.5.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 NCBI_TaxID=6239;
 [1]
 RN RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RC MEDLINE=92329978; PubMed=1627827;
 RA Smith M.J.;
 RT "A. C. elegans gene encodes a protein homologous to mammalian
 RT calreticulin".
 RL DNA Seq. 2:235-240(1992).
 [2]
 RN RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RC Baurer C., Courtney L., Laplant Y.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 [3]
 RN RN
 RP REVISIONS.
 RL Waterston R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: This protein binds calcium. There are both high and low
 CC affinity calcium-binding sites.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC SIMILARITY: Belongs to the calreticulin family.
 CC

RA Zupini A., Kaydamov C.;
 RT "Cloning and characterization of a cDNA encoding Chlamydomonas
 RL reinhardtii calreticulin";
 CC Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: This protein binds calcium. There are both high and low
 CC affinity calcium-binding sites (By similarity).
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
 CC -!- SIMILARITY: Belongs to the calreticulin family.
 CC
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 CC
 CC EMBL; AJ000765; CAB54526.1; -
 DR InterPro; IPR009033; Calret calnex P.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR008985; ConA like lec_gl.
 DR Pfam; PF00242; calreticulin; 1.
 DR PRSF; PRS002356; Calreticulin; 1.
 DR PRINTS; PR00626; Calreticulin; 1.
 DR PRODOM; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER TARGET; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 420 CALRETICULIN.
 FT SITE 417 420 PREVENT SECRETION FROM ER (POTENTIAL).
 FT SITE 417 420 PREVENT SECRETION FROM ER (POTENTIAL).
 SQ SEQUENCE 420 AA; 47327 MW; DD3BA3AFFBF61C9B CRC64;
 Query Match 53.6%; Score 208; DB 1; Length 420;
 Best Local Similarity 51.7%; Pred. No. 5.1e-18;
 Matches 37; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
 QY 1 CGGTGKVVHVFYKGNVLLINKDKDETHLVTLVIRPDNTVEYKIDNSQVESGSL 60
 DB 140 CGVSTRKVVHLYTKGNVLLIKDKAETDQLTHVTLVIRPDNTVEYKIDNSQVESGSL 199
 RESULT 13
 CRCTC BETVU STANDARD; PRT; 416 AA.
 ID CRCTC BETVU STANDARD; PRT; 416 AA.
 AC O81919;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Calreticulin precursor.
 OS Beta vulgaris (Sugar beet).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Amaranthaceae; Beta.
 OX NCBI_TaxID=161934;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VV-D/ZR5; TISSUE=Leaf;
 RA Viereck R.;
 RT "Nucleotide sequence from sugar beet calreticulin";
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: This protein binds calcium. There are both high and low
 CC affinity calcium-binding sites (By similarity).
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
 CC -!- SIMILARITY: Belongs to the calreticulin family.
 CC
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 CC
 CC EMBL; AJ002057; CAA05161.1; -
 DR PIR; T14554; T14554.
 DR InterPro; IPR009033; Calret calnex P.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR008985; ConA like lec_gl.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRSF; PRS002356; Calreticulin; 1.
 DR PRINTS; PR00826; Calreticulin; 1.
 DR PRODOM; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN_2; 1.
 DR PROSITE; PS00804; CALRETICULIN_REPEAT; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 416 CALRETICULIN.
 FT CARBOHYD 57 57 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 157 157 N-LINKED (GLCNAC...) (POTENTIAL).
 FT SITE 413 416 PREVENT SECRETION FROM ER (POTENTIAL).
 SQ SEQUENCE 416 AA; 48136 MW; 565FEC3469F77CA7 CRC64;
 Query Match 59.0%; Score 193; DB 1; Length 416;
 Best Local Similarity 56.7%; Pred. No. 3.5e-16;
 Matches 34; Conservative 9; Mismatches 17; Indels 0; Gaps 0;
 QY 1 CGGTGKVVHVFYKGNVLLINKDKDETHLVTLVIRPDNTVEYKIDNSQVESGSL 60
 DB 143 CGVSTRKVVHVFYKGNVLLINKDKDETHLVTLVIRPDNTVEYKIDNSQVESGSL 202
 RESULT 14
 CRCTC PRUAR STANDARD; PRT; 421 AA.
 ID CRCTC PRUAR STANDARD; PRT; 421 AA.
 AC Q9XF98;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Calreticulin precursor.
 OS Prunus armeniaca (Apicot).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 OX NCBI_TaxID=36596;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Bergeron; TISSUE=Endocarp, and Mesocarp;
 RA Mbeguie-A-Mbeguie D., Fils-Lycaon B.R.;
 RT "Molecular cloning and nucleotide sequence of a calreticulin from
 RT apricot (Prunus ameniaca cv. Bergeron)";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: This protein binds calcium. There are both high and low
 CC affinity calcium-binding sites (By similarity).
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
 CC -!- SIMILARITY: Belongs to the calreticulin family.
 CC
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 CC
 CC EMBL; AF134733; XAD32207.1; -
 DR InterPro; IPR009033; Calret calnex P.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR008985; ConA like lec_gl.
 DR InterPro; IPR008985; ER target_s.


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EMBL: U74831; AAB71420.1; -.
EMBL: U74830; AAB71419.1; -.
FIR: T10172; T10172.
InterPro: IPK009033; Calret_calmex_P.
InterPro: IPK01580; Calreticuliculin.
InterPro: IPK008985; ConA like lec_gl.
InterPro: IPK008986; ER_target_S.
Pfam: PF00262; calreticuliculin; 1.
PIRSE: PIRSEF002356; Calreticuliculin; 1.
PRINTS: PR00626; CALRETICULIN.
ProDom: PD001866; Calreticuliculin; 1.
PROSITE: PS00014; ER_TARGET; 1.
PROSITE: PS00803; CALRETICULIN 1; 1.
PROSITE: PS00804; CALRETICULIN 2; 1.

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OM protein - protein search, using sw model

Run on: October 4, 2004, 12:52:42 ; Search time 36.9588 Seconds
(without alignments)
520.758 Million cell updates/sec

Title: US-09-807-148-5
Perfect score: 327
Sequence: 1 CGPGTKKHVFNFKGNVL.....PNTYEVKIDNSQVSGSL 61

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL 25:.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_nhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	303	92.7	318	13 Q9PTX7	Q9ptx7 lampetra re
2	290	88.7	405	5 Q26268	Q26268 alysia cal
3	287	87.8	343	13 Q91711	Q91711 xenopus lae
4	287	87.8	411	13 Q91710	Q91710 xenopus lae
5	287	87.8	413	13 Q7ZW08	Q7zw08 xenopus lae
6	287	87.8	418	13 Q7ZYX3	Q7zyx3 xenopus lae
7	285	87.2	403	5 Q8T563	Q8t563 cotesia rub
8	284	86.9	407	5 Q8G672	Q8g672 dermacentor
9	280	85.6	406	5 Q8WR36	Q8wr36 anopheles g
10	279	85.3	421	5 Q8U6S0	Q8u6s0 strongyloce
11	278	85.0	406	5 Q9U916	Q9u916 drosophila
12	277	84.7	398	5 Q8G9E0	Q8g9e0 bombyx mori
13	277	84.7	398	5 Q7Z1E6	Q7z1e6 bombyx mori
14	276	84.4	397	5 Q8WPG8	Q8wpg8 gallieria me
15	276	84.4	410	5 Q16893	Q16893 amblyomma a
16	274	83.8	407	5 Q8T9U3	Q8t9u3 aedes aegypt

17 274 83.8 411 5 Q8MWP3
18 271 82.9 419 13 Q89884
19 268 82.0 417 13 Q9PUC1
20 265 81.0 423 13 Q7SZM3
21 263 80.4 417 13 Q802X3
22 258 78.9 387 5 Q97372
23 257 78.6 415 5 Q8MRU9
24 252 77.1 375 5 Q18478
25 249.5 76.3 403 5 Q76961
26 246 75.2 396 5 Q26514
27 246 75.2 396 5 Q45034
28 226 69.1 321 13 Q9USG0
29 218 66.7 395 5 Q96722
30 188 57.5 421 10 Q43712
31 188 57.5 442 10 Q7Y140
32 186 56.9 321 10 Q41799
33 185 56.6 412 10 Q40040
34 185 56.6 415 10 Q40041
35 183.5 56.1 427 10 Q9FYV2
36 183 56.0 425 10 Q8LJ85
37 182 55.7 137 11 Q9D373
38 182 55.7 272 11 Q8BL82
39 181 55.4 416 10 Q8H792
40 178 54.4 240 10 Q9ST29
41 178 54.4 389 10 Q40567
42 178 54.4 424 10 Q94AW7
43 178 54.4 424 10 Q8LC80
44 177 54.1 422 10 Q22502
45 176 53.8 380 10 Q7XAB5

ALIGNMENTS

RESULT 1

Q9PTX7 PRELIMINARY; PRT; 318 AA.

AC Q9PTX7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Calreticulin (Fragment).
OS Lampetra reissneri (Far Eastern brook lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Lethenteron.
OX NCBI_TaxID=7753;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2063780; PubMed=10594174;
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
genes.";
RL J. Mol. Evol. 49:729-735(1999).
DR EMBL; AB025328; BAA88481.1; -.
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret_cainex_P.
DR InterPro; IPR008985; ConA_like_rec_Gl.
DR InterPro; IPR000886; ER_target_S.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; 1.
FT NON TER
SQ SEQUENCE 318 AA; 36997 MW; C88102EALCACI506 CRC64;

Query Match 92.7%; Score 303; DB 13; Length 318;

Best Local Similarity 91.8%; Pred. No. 1.2e-27;

Matches 56; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGPGTKKHVFNFKGNVLINKDKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSL 60

Matches 54; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 CGPGTKKVVHVFNYKGNVLINKDIRCKDDSFTHLYTLIVRPDNTYEVKIDNSQVSGSL 60
DB 132 CGPPTKKVHVIFQYKKKNLQINKDIRCKDDSFTHLYTLIVRPDNTYEVKIDNSQVSGSL 191
QY 61 E 61
DB 192 E 192
RESULT 5
Q7ZWU8 PRELIMINARY; PRT; 413 AA.
AC Q7ZWU8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to calreticulin.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046699; AAH46699.1; -.
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret calnex P.
DR InterPro; IPR008985; ConA like lec_gl.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
SQ SEQUENCE 413 AA; 48521 MW; D8002F8F0523772B CRC64;
[1]
RP SEQUENCE FROM N.A.
Q7ZXV3 PRELIMINARY; PRT; 418 AA.
AC Q7ZXV3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to calreticulin.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
Query Match 87.8%; Score 287; DB 13; Length 413;
Best Local Similarity 88.5%; Pred. No. 1.3e-25;
Matches 54; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 CGPGTKKVVHVFNYKGNVLINKDIRCKDDSFTHLYTLIVRPDNTYEVKIDNSQVSGSL 60
DB 138 CGPPTKKVHVIFQYKKKNLQINKDIRCKDDSFTHLYTLIVRPDNTYEVKIDNSQVSGSL 197
QY 61 E 61
DB 198 E 198
RESULT 6
Q7ZXV3 PRELIMINARY; PRT; 418 AA.
AC Q7ZXV3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to calreticulin.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
Query Match 87.8%; Score 287; DB 13; Length 413;
Best Local Similarity 88.5%; Pred. No. 1.3e-25;
Matches 54; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 CGPGTKKVVHVFNYKGNVLINKDIRCKDDSFTHLYTLIVRPDNTYEVKIDNSQVSGSL 60
DB 138 CGPPTKKVHVIFQYKKKNLQINKDIRCKDDSFTHLYTLIVRPDNTYEVKIDNSQVSGSL 197
QY 61 E 61
DB 198 E 198

Klein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
EMBL; BC044068; AAH44068.1; -.
GO; GO:0005514; F:calcium ion storage activity; IEA.
InterPro; IPR001580; Calreticulin.
InterPro; IPR009033; Calret calnex P.
InterPro; IPR008985; ConA like lec_gl.
InterPro; IPR000886; ER_target_S.
Pfam; PF00262; calreticulin; 1.
PRINTS; PR00626; CALRETICULIN.
ProDom; PD001866; Calreticulin; 1.
PROSITE; PS00803; CALRETICULIN_1; 1.
PROSITE; PS00804; CALRETICULIN_2; 1.
PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
PROSITE; PS00014; ER_TARGET; 1.
PROSITE; PS00014; ER_TARGET; 1.
SEQUENCE 418 AA; 49028 MW; 731C1C9AA0BF9A53 CRC64;
Query Match 87.8%; Score 287; DB 13; Length 418;
Best Local Similarity 88.5%; Pred. No. 1.3e-25;
Matches 54; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 CGPGTKKVVHVFNYKGNVLINKDIRCKDDSFTHLYTLIVRPDNTYEVKIDNSQVSGSL 60
DB 138 CGPPTKKVHVIFQYKKKNLQINKDIRCKDDSFTHLYTLIVRPDNTYEVKIDNSQVSGSL 197
QY 61 E 61
DB 198 E 198
RESULT 7
Q8IS63 PRELIMINARY; PRT; 403 AA.
ID Q8IS63;
AC Q8IS63;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calreticulin.
DE Cotesia rubecula.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidea;
OC Braconidae; Microgasterinae; Cotesia.
OX NCBI_TaxID=32392;
RN [1]
RP SEQUENCE FROM N.A.
RA Asgari S., Zhang G., Schmidt O.;
RT "Polydnavirus particle proteins with similarities to molecular
RT chaparons, heat shock protein 70 and calreticulin."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; A150370; AAN73309.1; -.
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret calnex P.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR000886; ER_target_S.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
SEQUENCE 403 AA; 46550 MW; 259D771A822DB126 CRC64;
Query Match 87.2%; Score 285; DB 5; Length 403;
Best Local Similarity 83.6%; Pred. No. 2.1e-25;
Matches 51; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 CGPGTKKVVHVFNYKGNVLINKDIRCKDDSFTHLYTLIVRPDNTYEVKIDNSQVSGSL 60
DB 136 CGPPTKKVHVIFQYKKKNLQINKDIRCKDDSFTHLYTLIVRPDNTYEVKIDNSQVSGSL 195
QY 61 E 61

```
Db 196 E 196

RESULT 8
Q86G72 PRELIMINARY; PRT; 407 AA.
ID Q86G72 PRELIMINARY; PRT; 407 AA.
AC Q86G72;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Calreticulin.
OS Dermacentor variabilis.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Dermacentor.
OX NCBI_TaxID=34621;
RN [1]
RP SEQUENCE FROM N.A.
RA Simser J.A., Mulenga A., Macaluso K.R., Azad A.F.;
RT "Molecular characterization of Dermacentor variabilis calreticulin.";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY241957; AAC92278.1; -.
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret calnex P.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR00886; ER_target_S.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
SQ SEQUENCE 407 AA; 47190 MW; FFE063AC49446E8 CRC64;

Query Match 86.9%; Score 284; DB 5; Length 407;
Best Local Similarity 85.2%; Pred. No. 2.8e-25;
Matches 52; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRCKDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 60
Db 136 CGPGTKKHVIFNYKGNVLINKDIRCKDDVFTHTLVVRADNTYEVLDNEKVESGSL 195
QY 61 E 61
Db 196 E 196

RESULT 9
Q8WR36 PRELIMINARY; PRT; 406 AA.
ID Q8WR36 PRELIMINARY; PRT; 406 AA.
AC Q8WR36;
DT 01-VAR-2002 (TREMBlrel. 20, Created)
DT 01-VAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Calreticulin.
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=7165;
RN [1]
RP SEQUENCE FROM N.A.
RA Francischetti I.M., Valenzuela J.G., Ribeiro J.M.;
RT "Towards a catalog for genes and proteins from the salivary gland of
the malaria vector, Anopheles gambiae.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF457551; AAL68781.1; -.
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret calnex P.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR00886; ER_target_S.

Query Match 85.3%; Score 279; DB 5; Length 421;
Best Local Similarity 80.3%; Pred. No. 1.1e-24;
Matches 49; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRCKDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 60
Db 136 CGPGTKKHVIFNYKGNVLINKDIRCKDDVFTHTLVVRADNTYEVLDNEKVESGSL 195
QY 61 E 61
Db 196 E 196

RESULT 11
Q9U6S0 PRELIMINARY; PRT; 421 AA.
ID Q9U6S0 PRELIMINARY; PRT; 421 AA.
AC Q9U6S0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Calreticulin precursor.
CN CALRET.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RA Susan J.M., Just M.L., Lennarz W.J.;
RT "Cloning and Characterization of AlphaP Integrin and Calreticulin in
Embryos of the Sea Urchin.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF177915; AAD55725.1; -.
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret calnex P.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR00886; ER_target_S.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 1 19 POTENTIAL.
FT CHAIN 20 421 CALRETICULIN.
SQ SEQUENCE 421 AA; 48822 MW; 172C664F59F41F93 CRC64;

Query Match 85.3%; Score 279; DB 5; Length 421;
Best Local Similarity 80.3%; Pred. No. 1.1e-24;
Matches 49; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRCKDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 60
Db 136 CGPGTKKHVIFNYKGNVLINKDIRCKDDVFTHTLVVRADNTYEVLDNEKVESGSL 195
QY 61 E 61
Db 196 E 196

RESULT 11
```

Q9U916
ID Q9U916 PRELIMINARY; PRT; 406 AA.
AC Q9U916, 2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Calreticulin.
GN OS Drosophila melanogaster (fruit fly).
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP INTERPRO: IPR000886; ER_TARGET; 1.
RC STRAIN=OREGON-R;
RA Dodo X., Sakoyana Y., Gamo S.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
EMBL; AB000718; BAA85379.1; -;
DR FLYBase; FBgn0005585; Crc.
DR GO; GO:0007417; P:central nervous system development; IMP.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR003033; Calreticulin.
DR InterPro; IPR008985; ConA-like_lcc-gl.
DR InterPro; IPR008986; ER_target_S.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; 1.
SQ SEQUENCE 406 AA; 46809 MW; 68BA49A6B81CC427 CRC64;
Query Match 85.0%; Score 278; DB 5; Length 406;
Best Local Similarity 83.6%; Pred. No. 1.4e-24;
Matches 51; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CGPGTKKVVHVFNYKGNVLINCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSL 60
Db 137 CGPGTKKVVHVFNYKGNHLISKDKCKDDVYTHLYTLIVRPDNTYEVLDNKEVSGDL 196
Qy 61 E 61
Db 197 E 197
RESULT 12
Q869E0 PRELIMINARY; PRT; 398 AA.
ID Q869E0
AC Q869E0, 2000 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Calreticulin.
GN CRT.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP STRAIN=DAIZO; TISSUE=Fat body;
RC Takahashi T., Yamashita T.;
RL "Calreticulin expressed in fatbody of Bombyx mori.";
RT Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AB090887; BAC57964.1; -;
DR GO; GO:0005514; P:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR003033; Calreticulin.
DR InterPro; IPR008985; ConA-like_lcc-gl.
Q869E0 PRELIMINARY; PRT; 398 AA.
ID Q869E0
AC Q869E0, 2000 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Calreticulin.
GN CRT.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP STRAIN=DAIZO; TISSUE=Fat body;
RC Takahashi T., Yamashita T.;
RL "Calreticulin expressed in fatbody of Bombyx mori.";
RT Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AB090887; BAC57964.1; -;
DR GO; GO:0005514; P:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR003033; Calreticulin.
DR InterPro; IPR008985; ConA-like_lcc-gl.

DR InterPro; IPR000886; ER_target_S.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; 1.
SQ SEQUENCE 398 AA; 45768 MW; 522480CF9BD83306 CRC64;
Query Match 84.7%; Score 277; DB 5; Length 398;
Best Local Similarity 83.6%; Pred. No. 1.8e-24;
Matches 51; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
Qy 1 CGPGTKKVVHVFNYKGNVLINCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSL 60
Db 137 CGPGTKKVVHVFNYKGNHLISKDKCKDDVYTHLYTLIVRPDNTYEVLDNKEVSGDL 196
Qy 61 E 61
Db 197 E 197
RESULT 13
Q7Z1B6 PRELIMINARY; PRT; 398 AA.
ID Q7Z1B6
AC Q7Z1B6, 2000 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Calreticulin.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim S.R., Lee K.S., Kim I., Kang S.W., Nho S.K., Sohn H.D., Jin B.R.;
RT "Molecular cloning of a cDNA encoding putative calreticulin from the
RT silkworm, Bombyx mori.";
RL Int. J. Indust. Entomol. 6:93-97(2003).
DR EMBL; AY297158; AAP50845.1; -;
SQ SEQUENCE 398 AA; 45801 MW; 0BC049839F5950EA CRC64;
Query Match 84.7%; Score 277; DB 5; Length 398;
Best Local Similarity 83.6%; Pred. No. 1.8e-24;
Matches 51; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
Qy 1 CGPGTKKVVHVFNYKGNVLINCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSL 60
Db 137 CGPGTKKVVHVFNYKGNHLISKDKCKDDVYTHLYTLIVRPDNTYEVLDNKEVSGDL 196
Qy 61 E 61
Db 197 E 197
RESULT 14
Q8WPG8 PRELIMINARY; PRT; 397 AA.
ID Q8WPG8
AC Q8WPG8, 2000 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Calreticulin.
OS Galleria mellonella (Wax moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;
OC Pyralidae; Galleriinae; Galleria.
OX NCBI_TaxID=7137;
RN [1]
RP SEQUENCE FROM N.A.

GenCore version 5.1.6
Copyright (C) 1993 - 2004 Compugen Ltd.
QM protein - protein search, using sw model
Run on: October 4, 2004, 12:55:52 ; Search time 10.6647 Seconds
(without alignments)
441.961 Million cell updates/sec
Title: US-09-807-148-6
Perfect score: 258
Sequence: 1 NYKGNVLNKDIRCKDDDF.....PDNTYEVKIDNSQVESGSLE 49
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR 78 : *
1: pir1 : *
2: pir2 : *
3: pir3 : *
4: pir4 : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	258	100.0	416	1 S06763	calreticulin precu
2	258	100.0	416	2 JH0819	calreticulin precu
3	258	100.0	417	1 A37047	calreticulin precu
4	258	100.0	418	1 A34154	calreticulin precu
5	253	98.1	400	2 S43176	calreticulin, brai
6	253	98.1	421	2 S36799	calreticulin precu
7	226	87.6	384	2 S29130	calreticulin (clon
8	226	87.6	411	2 S29129	calreticulin precu
9	221	85.7	405	1 JH0795	calreticulin precu
10	210	81.4	419	2 S71343	calreticulin precu
11	209	81.0	406	2 A56637	calreticulin homol
12	182	70.5	336	2 A32507	41K larval antigen
13	182	70.5	393	1 A48573	calreticulin autoa
14	179	69.4	395	2 S25851	calreticulin precu
15	148	57.4	421	2 S58170	calreticulin precu
16	144	55.8	412	2 T05703	calreticulin - bar
17	144	55.8	415	2 T05705	calreticulin - bar
18	144	55.8	416	2 T14554	calreticulin - cas
19	143	55.4	415	2 T10172	calreticulin - cas
20	138	53.5	425	2 C36605	calreticulin (ortl
21	135	52.3	389	2 T03691	calreticulin - com
22	135	52.3	416	2 T16968	calreticulin cal
23	135	52.3	444	2 H56224	hypothetical prote
24	134	51.9	422	2 T07841	probable calreticu
25	101	39.1	591	2 B54354	calnexin precursor
26	101	39.1	591	2 B54354	calnexin precursor
27	101	39.1	592	2 I32260	calnexin - human
28	101	39.1	592	2 I46673	calnexin precursor
29	100	38.8	593	1 A37273	calnexin precursor

ALIGNMENTS

RESULT 1
S06763
calreticulin precursor - mouse
N:Alternate names: 55K calcium-binding reticuloplasmin; calregulin
C:Species: Mus musculus (house mouse)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S06763; JCI1444; PC1233; A57498
R:Smith, M.J.; Koch, G.L.E.
EMBO J. 8, 3581-3586, 1989
A:Title: Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a m
A:Reference number: S06763; MUID:90059955; PMID:2583110
A:Accession: S06763
A:Molecule type: DNA
A:Residues: 1-416 <SMI>
A:Cross-references: EMBL:X14926; NID:G50567; PIDN:CAA33053.1; PID:G50568
R:Mazzarella, R.A.; Gold, P.; Cunningham, M.; Green, M.
Gene 120, 217-225, 1992
A:Title: Determination of the sequence of an expressible cDNA clone encoding ERp60/calr
A:Reference number: JCI1444; MUID:93013037; PMID:1398135
A:Accession: JCI1444
A:Molecule type: mRNA
A:Residues: 1-416 <MAZ>
A:Cross-references: GB:M92988; NID:G193084; PIDN:AAA37569.1; PID:G193085
A:Accession: PC1233
A:Molecule type: protein
A:Residues: 18-41 <MA2>
R:White, T.K.; Zhu, Q.; Tanzer, M.L.
J. Biol. Chem. 270, 15926-15929, 1995
A:Title: Cell surface calreticulin is a putative mannoside lectin which triggers mouse
A:Reference number: A57498; MUID:95332280; PMID:7608143
A:Accession: A57498
A>Status: preliminary
A:Molecule type: protein
A:Residues: 74-80;142-151;186-193 <WHI>
C:Superfamily: calreticulin
C:Keywords: calcium binding
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-416/Product: calregulin #status experimental <MAT>
F:413-416/Region: endoplasmic reticulum retention signal
Query Match 100.0%; Score 258; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 5.2e-24;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYKGNVLNKDIRCKDDDFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 49
DB 149 NYKGNVLNKDIRCKDDDFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 197
RESULT 2
JH0819
calreticulin precursor - rat

calnexin precursor
calnexin homolog S
calmagin precursor
calnexin-t - mouse
calcium-binding pr
calnexin - human
calnexin homolog C
hypothetical prote
calnexin - soybean
calnexin-like prot
probable calnexin
calnexin - maize
site-specific DNA-
calnexin homolog -
synapsin IIb - num
hypothetical prote

N:Alternate names: calcium-binding protein 3
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Sep-1993 #sequence revision 20-Aug-1994 #text change 20-Jun-2000
 C:Accession: JH0819; A49176; S11205; PC1109; S45036; S04867; S39372; A34473; S13045
 R:Nakamura, M.; Moriya, M.; Baba, T.; Michikawa, Y.; Yamanobe, T.; Arai, K.; Okinaga, S.
 Exp. Cell Res. 205, 101-110, 1993
 A>Title: An endoplasmic reticulum protein, calreticulin, is transported into the acrosome
 A:Reference number: A49176; MUID:93202172; PMID:8453984
 A:Accession: JH0819
 A:Molecule type: mRNA
 A:Residues: 1-416 <NAK>
 A:Cross-references: GB:D78308; NID:G1089798; PIDN:BAAL11345.1; PID:G1845572
 A:Accession: A49176
 A>Status: preliminary
 A:Molecule type: mRNA; protein
 A:Residues: 1-416 <NA2>
 A:Cross-references: GB:D78308; NID:G1089798; PIDN:BAAL11345.1; PID:G1845572
 A:Experimental source: Sprague-Dawley, spermatogenic cells
 A:Note: sequence extracted from NCBI backbone (NCBIN:127639, NCBI:P:127643)
 R:Murthy, K.K.; Banville, D.; Srikanth, C.B.; Carrier, F.; Holmes, C.; Bell, A.; Patel, Y.
 Nucleic Acids Res. 18, 4933, 1990
 A>Title: Structural homology between the rat calreticulin gene product and the Onchoerca
 A:Reference number: S11205; MUID:90370496; PMID:2395661
 A:Accession: S11205
 A:Molecule type: mRNA
 A:Residues: 1-416 <MUR>
 A:Cross-references: EMBL:X53363; NID:G55854; PIDN:CAA37446.1; PID:G55855
 R:Nakamura, M.; Michikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.
 Biochem. Biophys. Res. Commun. 186, 668-673, 1992
 A>Title: Calreticulin is present in the acrosome of spermatozoa of rat testis.
 A:Reference number: PC1109; MUID:92360010; PMID:1497655
 A:Accession: PC1109
 A:Molecule type: protein
 A:Residues: 18-32 <NAK2>
 A:Experimental source: testis, strain Sprague-Dawley
 R:Soennichsen, B.; Fuellekrug, J.; van Nguyen, P.; Diekmann, W.; Robinson, D.G.; Mieskes
 submitted to the EMBL data library, May 1994
 A:Description: Retention and retrieval: both mechanisms cooperate to maintain calreticulin
 A:Reference number: S45036
 A:Accession: S45036
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-416 <SOE>
 A:Cross-references: EMBL:X79327; NID:G4988840; PIDN:CAA55890.1; PID:G4988941
 R:Jone, Y.C.; Bailly, A.; Laturuffe, N.
 submitted to the EMBL data library, December 1988
 A:Reference number: S04867
 A:Accession: S04867
 A:Molecule type: mRNA
 A:Residues: R' 270-358, 'AAG' <LON>
 A:Cross-references: EMBL:X13702; NID:G56055; PIDN:CAA31987.1; PID:G930260
 A:Note: the authors designated the protein as D-beta-hydroxybutyrate dehydrogenase
 R:Yokoi, T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horiuchi, R.; Kamataki, T.
 Biochim. Biophys. Acta 1158, 339-344, 1993
 A>Title: Identification of protein disulfide isomerase and calreticulin as autoimmunity an
 A:Reference number: S39371; MUID:94072621; PMID:8251535
 A:Accession: S39371
 A:Molecule type: protein
 A:Residues: 18-23, X', 25-32 <YOK>
 R:Van, P.N.; Peter, F.; Soeling, H.D.
 J. Biol. Chem. 264, 17494-17501, 1989
 A>Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes with
 active calcium sequestering rat liver vesicles
 A:Reference number: A34473; MUID:90008920; PMID:2793869
 A:Accession: A34473
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 18-36 <VAN>
 R:Trevies, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meld
 Biochem. J. 271, 473-480, 1990
 A>Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage
 A:Reference number: S13045; MUID:91054414; PMID:2241926
 A:Accession: S13045

A:Molecule type: protein
 A:Residues: 18-29 <TRB>
 C:Superfamily: calreticulin
 C:Keywords: calcium binding
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:18-416/Product: calreticulin #status experimental <MAT>
 F:204-212/Region: nuclear location signal
 F:413-416/Region: endoplasmic reticulum retention signal
 F:344/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 258; DB 2; Length 416;
 Best Local Similarity 100.0%; Pred. NO. 5.2e-24;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKRCKDETHLYTLIVRPDNTYEVKIDNSQVSGSLE 49
 |||||
 Db 149 NYKGNVLINKRCKDETHLYTLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 3

A37047
 calreticulin precursor - human
 N:Alternate names: 52K ribonucleoprotein autoantigen Ro/SS-A; 60K integrin-binding prote
 C:Species: Homo sapiens (man)
 C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 18-Feb-2000
 C:Accession: A42330; A37047; A46452; A28812; PH1525; A40346; S1475; T45075
 R:McCauffie, D.P.; Yang, Y.S.; Wilson, J.; Sontheimer, R.D.; Capra, J.D.
 J. Biol. Chem. 267, 2557-2562, 1992
 A>Title: The 5'-flanking region of the human calreticulin gene shares homology with the
 A:Reference number: A42330; MUID:92129342; PMID:1733953
 A:Accession: A42330
 A:Molecule type: DNA
 A:Residues: 1-417 <MC2>
 A:Note: sequence extracted from NCBI backbone (NCBIN:78537, NCBI:P:78536)
 R:McCauffie, D.P.; Lux, F.A.; Lieu, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachinski
 J. Clin. Invest. 85, 1379-1394, 1990
 A>Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/SS-
 A:Reference number: A37047; MUID:90237213; PMID:2332496
 A:Accession: A37047
 A:Molecule type: mRNA
 A:Residues: 1-417 <MCC>
 A:Cross-references: GB:M32294; NID:G337486; PIDN:AAA36582.1; PID:G337487
 A:Note: the authors translated the codon GTA for residue 349 as Tyr
 R:Rokeach, L.A.; Haselby, J.A.; Meilof, J.F.; Smeenk, R.J.; Unnasch, T.R.; Greene, B.M.;
 J. Immunol. 147, 3031-3039, 1991
 A>Title: Characterization of the autoantigen calreticulin.
 A:Reference number: A46452; MUID:92013129; PMID:1919005
 A:Accession: A46452
 A:Molecule type: mRNA
 A:Residues: 1-417 <ROK>
 A:Cross-references: GB:M84739; NID:G179881; PIDN:AAA51916.1; PID:G179882
 A:Note: sequence extracted from NCBI backbone (NCBIN:60749, NCBI:P:60750)
 R:Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sontheimer, R.D.
 J. Clin. Invest. 82, 96-101, 1988
 A>Title: Molecular characterization of human Ro/SS-A antigen. Amino terminal sequence of
 A:Reference number: A28812; MUID:88273610; PMID:3260607
 A:Accession: A28812
 A:Molecule type: protein
 A:Residues: 18-41 <LIE>
 A:Note: 18-Ala was also found
 R:Dupuis, M.; Schaefer, E.; Krause, K.H.; Tschopp, J.
 J. Exp. Med. 177, 1-7, 1993
 A>Title: The calcium-binding protein calreticulin is a major constituent of lytic granul
 A:Reference number: PH1525; MUID:93115648; PMID:8418194
 A:Accession: PH1525
 A:Molecule type: protein
 A:Residues: 18-27 <DUP>
 A:Experimental source: LAK cell
 R:Rojanian, M.V.; Finlay, B.B.; Gray, V.; Dedhar, S.
 Biochemistry 30, 9859-9866, 1991
 A>Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (calr
 A:Reference number: A40346; MUID:92002034; PMID:1911778
 A:Accession: A40346

A;Molecule type: protein
A;Residues: 18-34; R' <ROJ>
R;Krause, K.H.; Simmerman, H.K.B.; Jones, L.R.; Campbell, K.P.
Biochem. J. 270, 545-548, 1990
A;Title: Sequence similarity of calreticulin with a Ca(2+)-binding protein that co-purifies with the endoplasmic reticulum chaperone BiP
A;Reference number: S11475; MUID:90380058; PMID:2400400
A;Accession: S11475
A;Molecule type: protein
A;Residues: 18-32 <KRA>
R;Lamerdin, J.; McCreedy, P.; Stilwagen, S.; Ramirez, M.; Carrano, A.
Submitted to the EMBL Data Library, November 1996
A;Description: Characterization by genomic sequence analysis of a gene-rich 111 kb region on human chromosome 12p13.3
A;Reference number: Z22906
A;Accession: T45075
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-417 <LAM>
A;Cross-references: EMBL:AD000092; PIDN:AAB51176.1
A;Experimental source: cell line SHL2-B; fibroblast
A;Comment: Autoantibodies specific for this protein are found in Sjogren's syndrome and in other autoimmune diseases
C;Genetics:
A;Gene: GDB:CALR
A;Cross-references: GDB:125179; OMIM:109091
A;Map position: 19p13.3-19p13.2
A;Introns: 31/1; 65/1; 133/1; 164/3; 234/3; 272/3; 320/3; 351/3
A;Note: CRTC
C;Superfamily: calreticulin
C;Keywords: calcium binding; integrin binding
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-417/Product: calreticulin #status predicted <MAT>
F;414-417/Region: endoplasmic reticulum retention signal
Query Match 100.0%; Score 258; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.3e-24;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYKGNVLINKDIRCKDDEFTHTLVIRPDNTYEVKIDNSQVSGSLE 49
DB 149 NYKGNVLINKDIRCKDDEFTHTLVIRPDNTYEVKIDNSQVSGSLE 197
A;Molecule type: protein
A;Residues: 1-418 <FLI>
A;Cross-references: GB:J05138; NID:G164859; PIDN:AAA31188.1; PID:G164859
R;Treves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meldolesi, J.
Biochem. J. 271, 473-480, 1990
A;Title: Calreticulin is a candidate for a caldesmon-like function in Ca(2+)-storage
A;Reference number: S13045; MUID:91054414; PMID:2241926
A;Accession: S13047
A;Molecule type: protein
A;Residues: 19-32 <TR>
C;Superfamily: calreticulin
C;Keywords: skeletal muscle
F;1-17/Domain: signal sequence #status predicted <SIG>
F;415-418/Region: endoplasmic reticulum retention signal
Query Match 100.0%; Score 258; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 5.3e-24;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYKGNVLINKDIRCKDDEFTHTLVIRPDNTYEVKIDNSQVSGSLE 49

DB 149 NYKGNVLINKDIRCKDDEFTHTLVIRPDNTYEVKIDNSQVSGSLE 197
RESULT 5
S43376
calreticulin, brain isoform 1 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Oct-1994 #sequence_revision 23-Mar-1995 #text_change 07-May-1999
C;Accession: S43376; S36801
R;Matsuoka, K.; Seta, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isobe, T.
Biochem. J. 298, 435-442, 1994
A;Title: Covalent structure of bovine brain calreticulin.
A;Reference number: S43376; MUID:94183174; PMID:8135753
A;Accession: S43376
A;Molecule type: protein
A;Residues: 1-400 <MAT>
A;Experimental source: brain
R;Liu, N.; Fine, R.E.; Johnson, R.J.
Biochim. Biophys. Acta 1202, 70-76, 1993
A;Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin
A;Reference number: S36799; MUID:93385184; PMID:8373827
A;Accession: S36801
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 45-63; E', 65-83 <LIU>
A;Experimental source: brain, clone 8.1
C;Superfamily: calreticulin
C;Keywords: calcium binding; glycoprotein
F;137-400/Region: endoplasmic reticulum retention signal
F;120-146/Disulfide bonds: #status experimental
F;162/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 98.1%; Score 253; DB 2; Length 400;
Best Local Similarity 98.0%; Pred. No. 2.1e-23;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYKGNVLINKDIRCKDDEFTHTLVIRPDNTYEVKIDNSQVSGSLE 49
DB 132 NYKGNVLINKDIRCKDDEFTHTLVIRPDNTYEVKIDNSQVSGSLE 180
RESULT 6
S36799
calreticulin precursor, brain isoform 2 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Dec-1993 #sequence_revision 23-Mar-1995 #text_change 13-Aug-1999
C;Accession: S36799; S36800
R;Liu, N.; Fine, R.E.; Johnson, R.J.
Biochim. Biophys. Acta 1202, 70-76, 1993
A;Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin
A;Reference number: S36799; MUID:93385184; PMID:8373827
A;Accession: S36799
A;Molecule type: mRNA
A;Residues: 1-421 <LIU>
A;Cross-references: GB:J13462; NID:G348693; PIDN:AAC37307.1; PID:G348694
A;Experimental source: brain, clone 9.4
A;Accession: S36800
A;Molecule type: protein
A;Residues: 35-45 <LI2>
C;Superfamily: calreticulin
C;Keywords: calcium binding; glycoprotein
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-421/Product: calreticulin, brain isoform 2 #status predicted <MAT>
F;418-421/Region: endoplasmic reticulum retention signal
F;441-167/Disulfide bonds: #status predicted
F;193/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 98.1%; Score 253; DB 2; Length 421;
Best Local Similarity 98.0%; Pred. No. 2.2e-23;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYKGNVLINKDIRCKDDEFTHTLVIRPDNTYEVKIDNSQVSGSLE 49

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Db      153 NYKGNVLINKIRCKDDFTHTLYTLVIRPDNTYEVKIDNSQVSGSLE 201
|||||
RESULT 7
S29130
calreticulin (clone 8) - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: S29130; T01068
R:Treves, S.; Zorzato, F.; Pozzan, T.
Biochem. J. 287, 579-581, 1992
A:Title: Identification of calreticulin isoforms in the central nervous system.
A:Reference number: S29129; MUID:93074997; PMID:1445218
A:Accession: S29130
A:Molecule type: mRNA
A:Residues: 1-384 <TR>
A:CROSS-references: EMBL:X67598
A:Accession: T01068
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-339, 'XTGR' <TR>
A:CROSS-references: EMBL:X67598; NID:G64610; PIDN:CAA47867.1; PID:G64611
A:Experimental source: CNS
A:Superfamily: calreticulin
C:Keywords: glycoprotein
F:316/Binding site: carbohydate (Asn) (covalent) #status predicted
Query Match      87.6%; Score 226; DB 2; Length 384;
Best Local Similarity 89.6%; Pred. No. 4.2e-20;
Matches 43; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      2 YKGNVLINKIRCKDDFTHTLYTLVIRPDNTYEVKIDNSQVSGSLE 49
|||||
Db      122 YKKNLQINKIRCKDDSFTHLYTLVIRPDNTYEVKIDNSKVESGSLE 169
|||||

RESULT 8
S29129
calreticulin precursor (clone 3) - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: S29129
R:Treves, S.; Zorzato, F.; Pozzan, T.
Biochem. J. 287, 579-581, 1992
A:Title: Identification of calreticulin isoforms in the central nervous system.
A:Reference number: S29129; MUID:93074997; PMID:1445218
A:Accession: S29129
A:Molecule type: mRNA
A:Residues: 1-411 <TR>
A:CROSS-references: EMBL:X67597; NID:G64608; PIDN:CAA47866.1; PID:G64609
C:Superfamily: calreticulin
C:Keywords: glycoprotein
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F:13-411/Product: calreticulin #status predicted <MAT>
F:408-411/Region: endoplasmic reticulum retention signal
F:339/Binding site: carbohydate (Asn) (covalent) #status predicted
Query Match      87.6%; Score 226; DB 2; Length 411;
Best Local Similarity 89.6%; Pred. No. 4.5e-20;
Matches 43; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      2 YKGNVLINKIRCKDDFTHTLYTLVIRPDNTYEVKIDNSQVSGSLE 49
|||||
Db      145 YKKNLQINKIRCKDDSFTHLYTLVIRPDNTYEVKIDNSKVESGSLE 192
|||||

RESULT 9
JH0795
calreticulin precursor - California sea hare
N:Alternate names: protein 407
C:Species: Aplysia californica (California sea hare)

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C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0795; B31409; F60977
R:Kennedy, T.E.; Kuhl, D.; Barzilai, A.; Sweatt, J.D.; Kandel, E.R.
Neuron 9, 1013-1024, 1992
A:Title: Long-term sensitization training in aplysia leads to an increase in calreticulin
A:Reference number: JH0795; MUID:93098937; PMID:1463604
A:Accession: JH0795
A:Molecule type: mRNA
A:Residues: 1-405 <KEN>
A:CROSS-references: GB:S51239; NID:G262053; PIDN:AAB24569.1; PID:G262054
A:Experimental source: abdominal ganglion and antral nervous system
R:Kennedy, T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, E.R.; Sweatt, J.D.
Proc. Natl. Acad. Sci. U.S.A. 85, 7008-7012, 1988
A:Title: Sequencing of proteins from two-dimensional gels by using in situ digestion and
tion in Aplysia
A:Reference number: A94207; MUID:88320566; PMID:3413132
A:Accession: B31409
A:Molecule type: protein
A:Residues: 'X', 17-28, 'X', 30-31 <KE2>
R:Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl, K.
Electrophoresis 10, 152-157, 1989
A:Title: Development of a database of amino acid sequences for proteins identified and i
A:Reference number: A60977; MUID:89276284; PMID:2731514
A:Accession: F60977
A:Molecule type: protein
A:Residues: 'X', 17-28, 'X', 30-31 <SWE>
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-405/Product: calreticulin #status experimental <MAT>
F:402-405/Region: endoplasmic reticulum retention signal
Query Match      85.7%; Score 221; DB 1; Length 405;
Best Local Similarity 81.6%; Pred. No. 1.8e-19;
Matches 40; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      1 NYKGNVLINKIRCKDDFTHTLYTLVIRPDNTYEVKIDNSQVSGSLE 49
|||||
Db      145 NYKGNLQINKIRCKDDVFHSHLYTLVIRPDNTYEVKIDNKAESGDLE 193
|||||

RESULT 10
S71343
calreticulin precursor - Korean frog
C:Species: Rana rugosa (Korean frog)
C>Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 20-Jun-2000
C:Accession: S71343
R:Yamamoto, S.; Nakamura, M.
FEBS Lett. 387, 27-32, 1996
A:Title: Calnexin: its molecular cloning and expression in the liver of the frog, Rana r
A:Reference number: S71342; MUID:96234004; PMID:8654561
A:Accession: S71343
A:Molecule type: mRNA
A:Status: nucleic acid sequence not shown
A:Residues: 1-419 <YAM>
A:CROSS-references: EMBL:D78589; NID:G1514956; PIDN:BAAL1425.1; PID:G1514957
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-419/Product: calreticulin #status predicted <MAT>
F:205-213/Region: nuclear location signal
F:415-418/Region: endoplasmic reticulum retention signal
Query Match      81.4%; Score 210; DB 2; Length 419;
Best Local Similarity 81.6%; Pred. No. 4.3e-18;
Matches 40; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      1 NYKGNVLINKIRCKDDFTHTLYTLVIRPDNTYEVKIDNSQVSGSLE 49
|||||
Db      150 NYKGNLQINKIRCKADYVSHLYTLVIRPDNTYEVKIDNSKVESGNLE 198
|||||

RESULT 11

```

A;Molecule type: DNA
A;Residues: 91-105,'A',107,109-124;182-183,'L',185-220 <MCC>

RESULT 14
S25851
calreticulin precursor - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 06-Jan-1994 #sequence_revision 10-Nov-1995 #text_charge 05-Nov-1999
C.Accession: S25851; T33996
R:Smith, M.J
DNA Seq. 2, 235-240, 1992
A.Title: A C. elegans gene encodes a protein homologous to mammalian calreticulin.
A.Reference number: S25851; MUID:923299978; PMID:1627827

DNA Seq. 2, 235-240, 1992
 A; title: A. C. elegans gene encodes a protein homologous to mammalian calreticulin.
 A; Reference number: S25851; MUID:92329978; PMID:1627827
 A; Accession: S25851

A;Accession: U35536
A;Cross-references: EMBL:X59589; NID:g6693; PIDN:CAA42159.1; PID:g6694
R;Author: EMEL, L.; LaPlant, Y.
Submitted to the EMBL Data Library, February 1999
A;Description: The sequence of C. elegans cosmid Y38A10A.
A;Reference number: Z21453

A;Accession: T33996
 A;Status: preliminary; translated from GB/EMBL/DDBJ

A: Molecule type: DNA
A: Residues: 1-395 >BAU>
A: Cross-references: EMBL:AF125963; PID: AAD14746.1; GSPDB: GN00023; CESP: Y38A10A.5
A: Experimental source: Bristol N2: Clone Y38A10A

C>Genetics:
A>Gene: CBSP:Y38A10A.5
A>Map position: 5
A>Introns: 107/3: 315/3
C>Superfamily: calreticulin
F>1-15/Domain: signal sequence #status predicted <SIG>
F>332-395/Region: endoplasmic reticulum retention signal

C;Superfamily: calreticulin
F;1-15/Domain: signal sequence #status predicted <SIG>
F;392-395/Region: endoplasmic reticulum retention signal

Query Match	69.4%	Score 179;	DB 2;	Length 395;
Best Local Similarity	67.3%	Pred. No. 2.6e-14;		
Matches	33;	Conservative	5;	Mismatches 11;
				Indels 0;
				Gaps 0;

Qy 1 NYKGKVLINKDIRCKDDEFTHLYTLIVRPDNTEYVKIDNSQVESGSLE 49
 | | | : | | | | | | | | | | | | | | | |
Df 144 NYZGKNKIJKKETCKCSDELTHTYLILNSDPNTEYVKKIDGESAQTGSLE 192

RESULT 15

S58170 calreticulin precursor - maize
C|Species: Zea mays (maize)
C|Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 13-Aug-1999
C|Accession: S58170; S49818
R|Dresselhaus, T.; Hagel, C.; Loerz, H.; Kranz, E.
submitted to the EMBL Data Library, July 1995

A;Description: Isolation of a cDNA encoding Calreticulin from in vitro zygotes of maize.
A;Reference number: S58170
A;Accession: S58170
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-421 <PRE>
A;Cross-references: EMBL:X89813; NID:g927571; PIDN:CAA61939.1; PID:g927572
R;Napier, R.M.; Trueman, S.; Henderson, J.; Boyce, J.M.; Hawes, C.R.; Fricker, M.D.; Ven
submitted to the EMBL Data Library, November 1994
A;Description: Purification and sequencing of calreticulin from maize and evidence for it
A;Reference number: S49818
A;Accession: S49818
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-421 <NAP>
A;Cross-references: EMBL:Z46772; NID:g577611; PIDN:CAA86728.1; PID:g577612
C;Genetics:
A;Gene: CRT1
C;Superfamily: calreticulin
C;Keywords: calcium binding
F;1-25/Domain: signal sequence #status predicted <SIG>
F;418-421/Region: endoplasmic reticulum retention signal

Query Match 57.4%; Score 148; DB 2; Length 421;
Best Local Similarity 55.8%; Pred. No. 1.8e-10;
Matches 25; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 4 GKXVLKDKIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSL 48
Db 158 GKXHLIKDVPCETDQLTHTVYTLIRPDATYSLIDNEKQTGSI 202

Search completed: October 4, 2004, 13:06:35
Job time: 11.6647 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2004, 12:50:22 ; Search time 37.1824 Seconds
(without alignments)
372.349 Million cell updates/sec

Title: US-09-807-148-6

Perfect score: 258
Sequence: 1 NYKGRVLINKIRCKDEF.....PNTYEVKIDNSQVSGSLLE 49

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_29Jan04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	258	100.0	49	3 AAY92353	Aay92353 Recombina
2	258	100.0	60	3 AAY92354	Aay92354 Recombina
3	258	100.0	61	3 AAY92352	Aay92352 Recombina
4	258	100.0	180	3 AAY92351	Aay92351 Human vas
5	258	100.0	280	3 AAY92355	Aay92355 Recombina
6	258	100.0	400	3 AAY92350	Aay92350 Recombina
7	258	100.0	401	2 AAU11156	AAU11156 Calreticu
8	258	100.0	416	7 ADE56306	Ade56306 Rat Prote
9	258	100.0	416	7 ADE56310	Ade56310 Rat Prote
10	258	100.0	417	1 AAP92276	Aap92276 60 kD Ro
11	258	100.0	417	2 AAY00927	Aay00927 Calreticu
12	258	100.0	417	3 AAY92349	Aay92349 Human MBP
13	258	100.0	417	5 AAU77712	AAU77712 Human cal
14	258	100.0	417	5 AAU24591	AAU24591 Human cal
15	258	100.0	417	5 AAU18851	AAU18851 Human cal
16	258	100.0	417	5 ABB82384	ABB82384 Human cal
17	258	100.0	417	6 ABJ19766	ABJ19766 Human MP2
18	258	100.0	417	6 AAG79824	Aag79824 Calreticu
19	258	100.0	417	6 ADA26337	ADA26337 Human cal
20	258	100.0	417	7 ADD22407	ADD22407 HLA-B*46 T
21	258	100.0	417	7 ADE56308	Ade56308 Human Pro
22	258	100.0	417	7 ADE56312	Ade56312 Human Pro
23	218	84.5	403	2 AAU04171	AAU04171 Flea calr
24	209	81.0	406	4 ABB64414	Abb64414 Drosophil
25	190	73.6	122	2 AAY00926	Aay00926 Rat cc1qr

26	190	73.6	122	2 AAY00924	Aay00924 Human ccl
27	182	70.5	122	2 AAY00925	Aay00925 Mouse ccl
28	182	70.5	336	2 AAR12312	Aar12312 Partial s
29	145	56.2	385	3 AAB32385	Aab32385 Human sec
30	145	56.2	390	6 ABO07134	AbO07134 Novel hum
31	144	55.8	419	7 ABM74155	ABm74155 DNA clone
32	143	55.4	415	4 AAB66343	Aab66343 Castor be
33	143	55.4	415	4 AAB66341	Aab66341 Castor be
34	142	55.0	420	5 ABB04656	ABb04656 Maize cal
35	139	53.9	428	7 ABM74288	ABm74288 DNA clone
36	135	52.3	312	3 AAG47933	Aag47933 Arabidops
37	135	52.3	312	3 AAG24609	Aag24609 Arabidops
38	135	52.3	332	3 AAG30998	Aag30998 Arabidops
39	135	52.3	421	3 AAG24608	Aag24608 Arabidops
40	135	52.3	421	3 AAG47932	Aag47932 Arabidops
41	135	52.3	424	3 AAG24607	Aag24607 Arabidops
42	135	52.3	424	3 AAG47931	Aag47931 Arabidops
43	135	52.3	441	3 AAG30997	Aag30997 Arabidops
44	135	52.3	444	3 AAG30996	Aag30996 Arabidops
45	101	39.1	591	4 ABB44553	Abb44553 Mouse wou

ALIGNMENTS

RESULT 1

RAY92353

ID AAY92353 standard; protein; 49 AA.

XX

AC AAY92353;

XX

DT 10-AUG-2000 (first entry)

XX

DE Recombinant human calreticulin residues 132-180.

DE

KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermalogical; immunosuppressive; antiinflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

XX

OS Homo sapiens.

OS

CS Synthetic.

XX

PN WC200020577-A1.

XX

PD 13-APR-2000.

XX

PF 05-OCT-1999; 99WO-US023240.

XX

PR 06-OCT-1998; 98US-0103438P.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Tosato G, Pike SE, Yao L;

XX

WPI; 2000-303767/26.

DR

PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 useful for suppressing tumor growth.

XX

PS Claim 4; Page 82-83; 99pp; English.

XX

CC A novel method of inhibiting endothelial cell growth comprises contacting
 the cells with calreticulin (or its fragments/variants). Fragments of
 calreticulin causes at least 40% inhibition of angiogenesis, tumor growth
 and/or endothelial cell growth (claimed). The method may be used for
 inhibiting angiogenesis in a patient. The angiogenesis is associated with
 a disease other than a tumor that is associated with neovascularization
 (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular
 glaucoma, psoriasis, angiofibromas, immune inflammation,
 CC atherosclerosis, excessive wound repair, retinal neovascularization,
 CC macular degeneration, corneal graft rejection, contact lens overwear,
 CC Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic

CC lupus erythromatosus, thyroiditis, Goodpasture's syndrome, systemic
 CC vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary
 CC biliary cirrhosis). The method may also be used for treating/inhibiting
 CC tumor growth especially Kaposi's sarcoma (claimed)
 XX
 SQ Sequence 49 AA;

Query Match 100.0%; Score 258; DB 3; Length 49;
 Best Local Similarity 100.0%; Pred. No. 3.4e-31;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 49
 Db 1 NYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 49

RESULT 2

AA92354
 ID AAY92354 standard; protein; 60 AA.

AC AAY92354;

DT 10-AUG-2000 (first entry)

DE Recombinant human calreticulin residues 121-180.

KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

OS Homo sapiens.

OS Synthetic.

PN WO200020577-A1.

PD 13-APR-2000.

PF 05-OCT-1999; 99WO-US023240.

PR 06-OCT-1998; 98US-0103438P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Tosato G, Pike SE, Yao L;

XX WPI; 2000-303767/26.

XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 PT useful for suppressing tumor growth.

XX Claim 4; Page 85; 99pp; English.

XX A novel method of inhibiting endothelial cell growth comprises contacting
 CC the cells with calreticulin (or its fragments/variants). Fragments of
 CC calreticulin causes at least 40% inhibition of angiogenesis, tumor growth
 CC and/or endothelial cell growth (claimed). The method may be used for
 CC inhibiting angiogenesis in a patient. The angiogenesis is associated with
 CC a disease other than a tumor that is associated with neovascularization
 CC (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular
 CC glaucoma, psoriasis, angiofibromas, immune inflammation,
 CC atherosclerosis, excessive wound repair, retinal neovascularization,
 CC macular degeneration, corneal graft rejection, contact lens overwear,
 CC Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic
 CC lupus erythromatosus, thyroiditis, Goodpasture's syndrome, systemic
 CC vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary
 CC biliary cirrhosis). The method may also be used for treating/inhibiting
 CC tumor growth especially Kaposi's sarcoma (claimed)

XX Sequence 60 AA;

Query Match 100.0%; Score 258; DB 3; Length 60;
 Best Local Similarity 100.0%; Pred. No. 4.4e-31;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 49
 Db 12 NYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 60

RESULT 3

AA92352
 ID AAY92352 standard; protein; 61 AA.

AC AAY92352;

DT 10-AUG-2000 (first entry)

DE Recombinant human calreticulin residues 120-180.

KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

OS Homo sapiens.

OS Synthetic.

PN WO200020577-A1.

PD 13-APR-2000.

PF 05-OCT-1999; 99WO-US023240.

PR 06-OCT-1998; 98US-0103438P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Tosato G, Pike SE, Yao L;

XX WPI; 2000-303767/26.

XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 PT useful for suppressing tumor growth.

XX Claim 4; Page 82-83; 99pp; English.

XX A novel method of inhibiting endothelial cell growth comprises contacting
 CC the cells with calreticulin (or its fragments/variants). Fragments of
 CC calreticulin causes at least 40% inhibition of angiogenesis, tumor growth
 CC and/or endothelial cell growth (claimed). The method may be used for
 CC inhibiting angiogenesis in a patient. The angiogenesis is associated with
 CC a disease other than a tumor that is associated with neovascularization
 CC (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular
 CC glaucoma, psoriasis, angiofibromas, immune inflammation,
 CC atherosclerosis, excessive wound repair, retinal neovascularization,
 CC macular degeneration, corneal graft rejection, contact lens overwear,
 CC Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic
 CC lupus erythromatosus, thyroiditis, Goodpasture's syndrome, systemic
 CC vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary
 CC biliary cirrhosis). The method may also be used for treating/inhibiting
 CC tumor growth especially Kaposi's sarcoma (claimed)

XX Sequence 61 AA;

Query Match 100.0%; Score 258; DB 3; Length 61;
 Best Local Similarity 100.0%; Pred. No. 4.5e-31;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 49
 Db 13 NYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 61

RESULT 4

AA92351

ID AAY92351 standard; protein; 180 AA.
 AC AAY92351;
 XX
 DT 10-AUG-2000 (first entry)
 XX
 DE Human vasostatin (calreticulin N-terminal 180 amino acids).
 XX
 XX MBP-calreticulin; maltose binding protein; vasostatin; N-terminal;
 KW angiogenesis; inhibition; endothelial cell; anti-angiogenic;
 KW neuroprotective; antidiabetic; cytostatic; dermatological; hepatic;
 KW immunosuppressive; anti-inflammatory; anti-atherosclerotic;
 KW gastrointestinal; anti-arthritis; ophthalmic.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX WO200020577-A1.
 PN
 XX 13-APR-2000.
 PD
 XX 05-OCT-1999; 99WO-US023240.
 PF
 XX 06-OCT-1998; 98US-0103438P.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Tosato G, Pike SE, Yao L;
 PI WPI; 2000-303767/26.
 XX
 XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 PT useful for suppressing tumor growth.
 XX
 PS Claim 4; Page 82; 99pp; English.
 XX
 XX A novel method of inhibiting endothelial cell growth comprises contacting
 CC the cells with calreticulin (or its fragments/variants). Fragments of
 CC calreticulin causes at least 40% inhibition of angiogenesis, tumor growth
 CC and/or endothelial cell growth (claimed). The method may be used for
 CC inhibiting angiogenesis in a patient. The angiogenesis is associated with
 CC a disease other than a tumor that is associated with neovascularization
 CC (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular
 CC glaucoma, psoriasis, angiofibromas, immune inflammation,
 CC atherosclerosis, excessive wound repair, retinal neovascularization,
 CC macular degeneration, corneal graft rejection, contact lens overwear,
 CC Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic
 CC lupus erythematous, thyroiditis, Goodpasture's syndrome, systemic
 CC vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary
 CC biliary cirrhosis). The method may also be used for treating/inhibiting
 CC tumor growth especially Kaposi's sarcoma (claimed)
 XX
 SQ Sequence 180 AA;
 Query Match 100.0%; Score 258; DB 3; Length 180;
 Best Local Similarity 100.0%; Pred. No. 1.9e-30;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NYGKGNVLINKDKDDEFTHTLVLPDNTYEVKIDNSQVSGSLE 49
 |||||
 DB 132 NYGKGNVLINKDKDDEFTHTLVLPDNTYEVKIDNSQVSGSLE 180
 |||||
 RESULT 5
 AAY92355
 ID AAY92355 standard; protein; 280 AA.
 XX
 AC AAY92355;
 XX
 DT 10-AUG-2000 (first entry)
 XX
 DE Recombinant delta-120 calreticulin.
 XX

KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermatological; immunosuppressive; anti-inflammatory; hepatic;
 XX anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
 OS Homo sapiens.
 OS Synthetic.
 XX WO200020577-A1.
 PN
 XX 13-APR-2000.
 PD
 XX 05-OCT-1999; 99WO-US023240.
 PF
 XX 06-OCT-1998; 98US-0103438P.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Tosato G, Pike SE, Yao L;
 PI WPI; 2000-303767/26.
 XX
 XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 PT useful for suppressing tumor growth.
 XX
 PS Claim 4; Page 86; 99pp; English.
 XX
 XX This sequence comprises recombinant human calreticulin (AAY92350) missing
 CC the N-terminal 120 amino acids. A novel method of inhibiting endothelial
 CC cell growth comprises contacting the cells with calreticulin (or its
 CC fragments/variants). Fragments of calreticulin causes at least 40%
 CC inhibition of angiogenesis, tumor growth and/or endothelial cell growth
 CC (claimed). The method may be used for inhibiting angiogenesis in a
 CC patient. The angiogenesis is associated with a disease other than a tumor
 CC that is associated with neovascularization (e.g. diabetic neuropathy,
 CC retrolental fibroplasia, trachoma, neovascular glaucoma, psoriasis,
 CC angiofibromas, immune inflammation, atherosclerosis, excessive wound
 CC repair, retinal neovascularization, macular degeneration, corneal graft
 CC rejection, contact lens overwear, Crohn's disease, non-immune
 CC inflammation, rheumatoid arthritis, systemic lupus erythematous,
 CC thyroiditis, Goodpasture's syndrome, systemic vasculitis, scleroderma,
 CC Sjorgen's syndrome, sarcoidosis and primary biliary cirrhosis). The
 CC method may also be used for treating/inhibiting tumor growth especially
 CC Kaposi's sarcoma (claimed)
 XX
 SQ Sequence 280 AA;
 Query Match 100.0%; Score 258; DB 3; Length 280;
 Best Local Similarity 100.0%; Pred. No. 3.4e-30;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NYGKGNVLINKDKDDEFTHTLVLPDNTYEVKIDNSQVSGSLE 49
 |||||
 DB 12 NYGKGNVLINKDKDDEFTHTLVLPDNTYEVKIDNSQVSGSLE 60
 |||||
 RESULT 6
 AAY92350
 ID AAY92350 standard; protein; 400 AA.
 XX
 AC AAY92350;
 XX
 DT 10-AUG-2000 (first entry)
 XX
 DE Recombinant human MBP-calreticulin.
 XX
 KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermatological; immunosuppressive; anti-inflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
 XX
 OS Homo sapiens.
 OS

CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 416 AA;

SQ Query Match 100.0%; Score 258; DB 7; Length 416;
 Best Local Similarity 100.0%; Pred. No. 5,7e-30;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDDETHLYTLVLRPDNTYEVKIDNSQVESGSLE 49
 Db 149 NYKGNVLINKDIRCKDDETHLYTLVLRPDNTYEVKIDNSQVESGSLE 197

RESULT 9

AD56310
 ID ADE56310 standard; protein; 416 AA.

XX ADE56310;

XX 29-JAN-2004 (first entry)

XX Rat Protein P18418, SEQ ID NO 2162.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX Rattus norvegicus.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GEHO) GEN HOSPITAL CORP.

XX (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

DR WPI; 2003-268312/26.

DR GENBANK; F18418.

XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell

CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 416 AA;

SQ Query Match 100.0%; Score 258; DB 7; Length 416;
 Best Local Similarity 100.0%; Pred. No. 5,7e-30;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDDETHLYTLVLRPDNTYEVKIDNSQVESGSLE 49
 Db 149 NYKGNVLINKDIRCKDDETHLYTLVLRPDNTYEVKIDNSQVESGSLE 197

RESULT 10

AAP2276
 ID AAP2276 standard; protein; 417 AA.

XX AAP2276;

XX 25-MAR-2003 (revised)

DT 23-FEB-1990 (first entry)

XX 60 kD Ro (Ro/SSA) antigen.

XX Sjorens syndrome; systemic lupus erythematosus.

XX Synthetic.

XX WO8909273-A.

XX 05-OCT-1989.

XX 22-MAR-1989; 89WO-US001213.

XX 22-MAR-1988; 88US-00171634.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Sontheimer RD, Lieu TS, Capra JD, Mccaullife DP;

XX WPI; 1989-309537/42.

DR N-PSDB; AAP2276.

XX DNA sequences encoding antigenic epitope(s) of RO 60 KD auto-antigen -
 PT used in immunoassays to detect rheumatic disease.

XX Disclosure; Fig 2; 88pp; English.

XX Synthetic peptides corresp. to an epitopic core of Ro antigen are
 CC expressed recombinantly to detect autoantibodies, for identification of
 CC autoimmune diseases. These epitopes are AAS 24-36, 23-36, 188-209, or 241

CC -255. The peptides may be substd. for ribonucleoprotein particle
 CC antigens. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-
 CC MAR-2003 to correct PI field.)
 XX
 SQ Sequence 417 AA;

Query Match 100.0%; Score 258; DB 1; Length 417;
 Best Local Similarity 100.0%; Pred. No. 5.7e-30;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKIRCKDDFTHLYTLIVRPDNTYEVKIDNSQVSGSLE 49
 DB 149 NYKGNVLINKIRCKDDFTHLYTLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 11
 AAY00927
 ID AAY00927 standard; protein; 417 AA.
 XX
 AC AAY00927;
 XX
 DT 28-MAY-1999 (first entry)
 XX
 DE Calreticulin.

XX C1q and collectin receptor; cC1qR binding domain; complement ubiquitin;
 XX CUB functionality; inhibitor; complement activation; inflammation;
 KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
 KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
 KW immune complex nephritis; therapy.
 XX
 OS Homo sapiens.
 XX
 FN WO9907406-A1.
 XX
 PD 18-FEB-1999.
 XX
 PF 12-AUG-1998; 98WO-GE02430.
 XX
 PR 12-AUG-1997; 97GB-00016998.
 XX
 PA (UYLE-) UNIV LEICESTER.
 XX
 PI Schwaebler W;
 XX
 DR WPI; 1999-180404/15.

XX Use of a cC1qR binding domain - to modulate complement ubiquitin (CUB)
 XX functionality.
 XX
 PS Disclosure; Page 26-27; 31pp; English.
 XX
 CC This sequence is calreticulin, a homologue of C1q and collectin receptor
 CC (cC1qR). The invention relates to the use of a cC1qR binding domain in a
 CC medicament to effect complement ubiquitin (CUB) functionality, and an
 CC inhibitor of the cC1qR binding domain in a medicament to inhibit CUB
 CC functionality. The cC1qR binding domain, or its inhibitor, can be used to
 CC treat a human or animal body. Particularly an inhibitor is used to treat
 CC complement activation involved in the initiation and maintenance of
 CC inflammation, for example in myocardial infarction, brain ischaemia
 CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus
 CC erythematosus, burns, immune complex nephritis, and to treat amyloid
 CC plaques in Alzheimer's disease. The use of cC1qR binding domain or
 CC inhibitor enables the CUB domain functionality to be modulated using a
 CC low molecular weight molecule
 XX
 SQ Sequence 417 AA;

Query Match 100.0%; Score 258; DB 2; Length 417;
 Best Local Similarity 100.0%; Pred. No. 5.7e-30;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKIRCKDDFTHLYTLIVRPDNTYEVKIDNSQVSGSLE 49

DB 149 NYKGNVLINKIRCKDDFTHLYTLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 12
 AAY92349
 ID AAY92349 standard; protein; 417 AA.
 XX
 AC AAY92349;
 XX
 DT 10-AUG-2000 (first entry)
 XX
 DE Human MBP-calreticulin.

XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermalogical; immunosuppressive; anti-inflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
 XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT Peptide 1..17
 FT Protein /label= signal_peptide
 FT Protein 18
 FT Protein /label= mature_protein
 XX WO200020577-A1.
 XX
 PD 13-APR-2000.

XX
 PF 05-OCT-1999; 99WO-US023240.
 XX
 PR 06-OCT-1998; 98US-0103438P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Tosato G, Pike SE, Yao L;
 XX WPI; 2000-303767/26.
 DR N-PSDB; AAA09346, AAA09347.
 XX
 PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 PT useful for suppressing tumor growth.
 XX
 PS Disclosure; Page 79-80; 99pp; English.

XX A novel method of inhibiting endothelial cell growth comprises contacting
 CC the cells with calreticulin (or its fragments/variants). Fragments of
 CC calreticulin causes at least 40% inhibition of angiogenesis, tumor growth
 CC and/or endothelial cell growth (claimed). The method may be used for
 CC inhibiting angiogenesis in a patient. The angiogenesis is associated with
 CC a disease other than a tumor that is associated with neovascularization
 CC (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular
 CC glaucoma, psoriasis, angiofibromas, immune inflammation,
 CC atherosclerosis, excessive wound repair, retinal neovascularization,
 CC macular degeneration, corneal graft rejection, contact lens overwear,
 CC Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic
 CC lupus erythematosus, thyroiditis, Goodpasture's syndrome, systemic
 CC vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary
 CC biliary cirrhosis). The method may also be used for treating/inhibiting
 CC tumor growth especially Kaposi's sarcoma (claimed)

XX Sequence 417 AA;

Query Match 100.0%; Score 258; DB 3; Length 417;
 Best Local Similarity 100.0%; Pred. No. 5.7e-30;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKIRCKDDFTHLYTLIVRPDNTYEVKIDNSQVSGSLE 49
 DB 149 NYKGNVLINKIRCKDDFTHLYTLIVRPDNTYEVKIDNSQVSGSLE 197

cancer; autoimmune disease; viral infection; cardiovascular disease;
antitense therapy; cytostatic; immunosuppressive; virucide.
Homo sapiens.
WQ200236743-A2.
10-MAY-2002.
30-OCT-2001; 2001WO-US049045.
30-OCT-2000; 2000US-00702327.
30-OCT-2000; 2000US-00702327.
(ISIS-) ISIS PHARM INC.
Bennett CF, Cowser LM;
WPI; 2002-479759/51.
N-PSDB; AAD39469.
Novel antisense compound targeted to nucleic acid encoding calreticulin,
useful for treating a human having disease or condition associated with
calreticulin e.g. cancer, viral infection, autoimmune disease.
Disclosure; Page 88-90; 109pp; English.
The invention relates to antisense compounds, compositions and methods
for modulating the expression of calreticulin. The compositions comprise
antisense compounds, particularly antisense oligonucleotides, targeted
to nucleic acids encoding calreticulin. The antisense compound is useful
for inhibiting the expression of calreticulin in human cells or tissues.
It is also useful for treating a human having a disease or condition
associated with calreticulin, e.g., hyperproliferative disorder e.g.
cancer, autoimmune disease, viral infection or cardiovascular disease, by
inhibiting expression of calreticulin. It is useful for diagnostics,
therapeutics, prophylaxis and as research reagents and kits. It is also
used in antisense therapy. The present sequence is human calreticulin
protein. This sequence is used in the exemplification of the invention

Sequence 417 AA;

Query March 100.0%; Score 258; DB 5; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.7e-30;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Oy 1 NYKGNVLINKDIRCKDDETHLYTLIVRPNTYEVKIDNSQVSGSLE 49
|||||
Db 149 NYKGNVLINKDIRCKDDETHLYTLIVRPNTYEVKIDNSQVSGSLE 197
|||||

RESULT 15
AAE18851
ID AAE18851 standard; protein; 417 AA.
XX AAE18851;
XX
DT 17-MAY-2002 (first entry)
XX Human calreticulin protein.
DE
XX Human; prostate cancer; calreticulin; T1D-1 protein; TRAITS protein;
KW androgen action pathway; cell proliferation; kidney cancer; lymphoma;
KW epithelium-derived carcinoma; leukaemia; vaccine; gene therapy;
KW cytostatic; U19 protein.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH Domain /label= N-terminal_domain
FT FT 98..170
FT Region 98..103
FT FT /label= Alpha_helix
FT FT 149..154

```

RESULT 13
AAU77712
AAU77712 standard; protein; 417 AA.
XX
XX
AAU77712;
XX
05-JUN-2002 (first entry)
XX
Human calreticulin (CRT).
XX
Calreticulin; CRT; endoplasmic reticulum chaperone polypeptide;
XX
cytostatic; vaccine; human papillomavirus 16; HPV 16; E7; DNA vaccine;
XX
enhanced antigen-specific immune response; cytotoxic T lymphocyte;
XX
tumour; cancer; cervical cancer.
XX
XX
Homo sapiens.
XX
WO200212281-A2.
XX
14-FEB-2002.
XX
02-AUG-2001; 2001WO-US024134.
XX
03-AUG-2000; 2000US-0222902P.
XX
(UYJO ) UNIV JOHNS HOPKINS.
XX
Wu T, Hung C;
XX
WPI: 2002-257463/30.
XX
N-PSDB; ABK11662.
XX
New nucleic acids encoding a fusion polypeptide comprising an endoplasmic
XX
reticulum chaperone polypeptide linked to an antigenic polypeptide,
XX
useful as a vaccine for inducing antigen-specific immune responses.
XX
Disclosure; Page 27; 71pp; English.
XX
The invention describes a nucleic acid molecule (I) encoding a fusion
XX
polypeptide comprising a first polypeptide domain comprising an
XX
endoplasmic reticulum chaperone polypeptide e.g. calreticulin (CRT) and a
XX
second polypeptide domain comprising at least one antigenic peptide e.g.
XX
Human papillomavirus 16 (HPV 16) E7. The nucleic acid is useful as a
XX
vaccine (DNA vaccine) for inducing enhanced antigen-specific immune
XX
responses, particularly for those mediated by cytotoxic T lymphocytes. The
XX
nucleic acid and compositions comprising the nucleic acid is also useful
XX
for inhibiting the growth of tumours and cancers e.g. cervical cancer.
XX
This is the amino acid sequence of the human calreticulin (CRT), an
XX
endoplasmic reticulum protein used in the creation of a DNA vaccine
XX
Sequence 417 AA;
XX
Query Match 100.0%; Score 258; DB 5; Length 417;
XX
Best Local Similarity 100.0%; Fred. No. 5.7e-30;
XX
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
QY 1 NYKGKVLINKDIRCKDDEFTHLTYLIVRPDNTVEYKIDNSQVSGSL 49
XX
149 NYKGKVLINKDIRCKDDEFTHLTYLIVRPDNTVEYKIDNSQVSGSL 197
XX
DB5
XX
RESULT 14
AAE24591
AAE24591 standard; protein; 417 AA.
XX
XX
AAE24591;
XX
XX
04-OCT-2002 (first entry)
XX
Human calreticulin protein.
XX
Human; calreticulin; antitense compound; hyperproliferative disorder;

```

```

FT      /label= Alpha_helix
FT      171..285
FT      /note= "Proline-rich domain (P domain)"
FT      286..397
FT      /label= C-terminal_domain
XX      WO200206327-A2.
XX      24-JAN-2002.
XX      17-JUL-2001; 2001WO-US022357.
XX      17-JUL-2000; 2000US-0218761P.
XX      16-JUL-2001; 2001US-00906393.
XX      (NOUN ) UNIV NORTHWESTERN.
XX      Wang Z, Xiao W;
XX      WPI; 2002-179780/23.
XX      N-PSDB; AAD29931.
XX      Identifying a subject that is likely to have aggressive form of prostate
XX      cancer, involves comparing calreticulin levels in prostate specimen of
XX      the subject and in benign prostatic epithelial cells of the same subject.
XX      Disclosure; Page 146-148; 148pp; English.
XX      The present invention relates to methods of distinguishing aggressive
XX      forms of prostate cancer from non-aggressive forms. The method involves
XX      comparing the level of calreticulin in prostate specimen and in benign
XX      prostatic epithelial cells of a subject. The invention particularly
XX      relates to two proteins, namely calreticulin and T1D-1 (TRAITS; U19) that
XX      are down-regulated in aggressive forms of prostate cancer but not in
XX      slowly progressing prostate cancer. They play important roles in the part
XX      of androgen action pathway that suppresses cell proliferation and/or
XX      prevents prostate cancer. The method is useful for identifying a subject
XX      who is likely to have an aggressive form of prostate cancer. The
XX      invention further relates to a method of identifying a subject with a
XX      slow growing form of prostate cancer. T1D-1 sequences are useful for
XX      treating cancers such as epithelium-derived carcinomas, kidney cancers,
XX      lymphomas, leukaemias and prostate cancers. Sequences of the invention
XX      are used as vaccines and in gene therapy. The present sequence is human
XX      calreticulin protein
XX      SQ      Sequence 417 AA;
XX      Query Match      100.0%; Score 258; DB 5; Length 417;
XX      Best Local Similarity 100.0%; Pred. No. 5.7e-30;
XX      Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX      QY      1 NYKGNVLINKDIRCKDDEFTLYLIVRPONTVEVKIDNSQVSGSLE 49
XX      Db      149 NYKGNVLINKDIRCKDDEFTLYLIVRPONTVEVKIDNSQVSGSLE 197

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Search completed: October 4, 2004, 13:03:31
 Job time : 37.1824 secs

Sequence 4, Appli
Sequence 7004, Ap
Sequence 41, Appl
Sequence 41, Appl
Sequence 8, Appli
Sequence 4459, Ap
Sequence 3, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 15, Appli
Sequence 2, Appli
Sequence 5080, Ap
Sequence 13, Appl
Sequence 7, Appli
Sequence 54, Appl
Sequence 54, Appl
Sequence 54, Appl

US-09-784-508-4
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US-08-456-647B-41
US-08-237-401A-41
US-09-700-397-8
US-09-134-001C-4469
US-08-752-238-3
US-09-085-603B-3
US-09-031-897-7
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US-08-336-447A-15
US-09-091-117-2
US-09-134-001C-5080
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US-08-419-652-7
US-08-190-802A-54
US-08-477-346-54
US-08-473-089-54

28 52.5 20.3 358 4
29 52 20.2 116 4
30 51.5 20.0 54 2
31 51.5 20.0 54 2
32 51 19.8 478 4
33 50.5 19.6 513 4
34 50.5 19.6 599 1
35 50.5 19.6 599 3
36 50.5 19.6 599 3
37 50.5 19.6 599 4
38 50 19.4 889 4
39 50 19.4 1030 3
40 50 19.4 3696 4
41 49.5 19.2 238 2
42 49.5 19.2 620 2
43 49.5 19.2 816 1
44 49.5 19.2 816 3
45 49.5 19.2 816 4

ALIGNMENTS

RESULT 1
US-09-828-000-8
; Sequence 8, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Fragment 5
US-09-828-000-8

Query Match 100.0%; Score 258; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 3.2e-30;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKIRCKDDEFFHLYTLIVRPDNTYEVKIDNSQVESGSLE 49
DB 13 NYKGNVLINKIRCKDDEFFHLYTLIVRPDNTYEVKIDNSQVESGSLE 61

RESULT 2
US-09-828-000-3
; Sequence 3, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Vasostatin
US-09-828-000-3

Query Match 100.0%; Score 258; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.3e-29;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKIRCKDDEFFHLYTLIVRPDNTYEVKIDNSQVESGSLE 49

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OM protein - protein search, using sw model

Run on: October 4, 2004, 13:01:22 ; Search time 10.9529 Seconds
(without alignments)
230.958 Million cell updates/sec

Title: US-09-807-148-6
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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	258	100.0	61	4	US-09-828-000-8
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3	258	100.0	416	4	US-09-828-000-2
4	175	67.8	35	4	US-09-828-000-7
5	175	67.8	61	4	US-09-828-000-4
6	143	55.4	415	3	US-08-675-816-2
7	100	38.8	593	1	US-08-296-362-2
8	95	36.8	610	4	US-09-976-594-947
9	82	31.8	18	4	US-09-828-000-6
10	82	31.8	27	4	US-09-828-000-5
11	68	26.4	542	3	US-08-675-816-6
12	61.5	23.8	582	3	US-08-906-865-3
13	61.5	23.8	582	4	US-09-129-668-3
14	55	21.3	588	4	US-09-252-991A-18861
15	54	20.9	405	1	US-07-829-954-2
16	54	20.9	405	1	US-07-994-423-2
17	54	20.9	405	1	US-08-421-891-2
18	53.5	20.7	279	4	US-08-701-191A-23
19	53.5	20.7	279	4	US-09-664-526-23
20	53.5	20.7	355	1	US-08-292-549-6
21	53.5	20.7	355	3	US-09-006-353A-14
22	53.5	20.7	355	4	US-09-573-986-14
23	53.5	20.7	943	4	US-09-540-236-3458
24	53.5	20.7	984	2	US-08-673-789-9
25	53.5	20.7	984	2	US-08-449-645A-19
26	53.5	20.7	984	2	US-08-702-367A-19
27	53.5	20.7	984	5	PCT-US95-04681-19

Db 132 NYKGNVLINKDIRCKDDEFTHTLYTLVDPNTYEVKIDNSQVSGSLE 180
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RESULT 3

US-09-828-000-2
; Sequence 2, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Calreticulin
US-09-828-000-2

Query Match 100.0%; Score 258; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 3.8e-29;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDDEFTHTLYTLVDPNTYEVKIDNSQVSGSLE 49
Db 149 NYKGNVLINKDIRCKDDEFTHTLYTLVDPNTYEVKIDNSQVSGSLE 197
|||||

RESULT 4

US-09-828-000-7
; Sequence 7, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Fragment 4
US-09-828-000-7

Query Match 67.8%; Score 175; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.7e-18;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDDEFTHTLYTLVDPN 32
Db 4 NYKGNVLINKDIRCKDDEFTHTLYTLVDPN 35
|||||

RESULT 5

US-09-828-000-4
; Sequence 4, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4
; LENGTH: 61
; TYPE: PRT

; ORGANISM: Fragment 1
US-09-828-000-4

Query Match 67.8%; Score 175; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 3.5e-18;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDDEFTHTLYTLVDPN 32
Db 30 NYKGNVLINKDIRCKDDEFTHTLYTLVDPN 61
|||||

RESULT 6

US-08-675-816-2
; Sequence 2, Application US/08675816
; Patent No. 6171864
; GENERAL INFORMATION:
; APPLICANT: Coughlan, Sean J.
; APPLICANT: Winfrey, Jr., Ron J.
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 701 Fifth Ave. Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,816
; FILING DATE: 05-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6171864tenburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 750027.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)-622-4900
; TELEFAX: (206)-682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-675-816-2

Query Match 55.4%; Score 143; DB 3; Length 415;
Best Local Similarity 50.0%; Pred. No. 1.8e-12;
Matches 24; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDDEFTHTLYTLVDPNTYEVKIDNSQVSGSL 48
Db 150 NYNDTHLIKKEVPCEPDTOLTHVYTLVIRPDATYSLIDNVEKQTGSL 197
|||||

RESULT 7

US-08-296-362-2
; Sequence 2, Application US/08296362
; Patent No. 5691306
; GENERAL INFORMATION:
; APPLICANT: Bergeron, John J.M.
; APPLICANT: Thomas, David Y.
; APPLICANT: Wada, Ikuo
; TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF
; TITLE OF INVENTION: PROTEIN TRAPPING DISORDERS AND INCREASING SECRETORY
; NUMBER OF SEQUENCES: 2

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,816
FILING DATE: 05-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6171864tenburg, Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 750027.401
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)-622-4900
TELEFAX: (206)-682-6031
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 542 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-675-816-6

Query Match 26.4%; Score 68; DB 3; Length 542;
Best Local Similarity 40.0%; Pred. No. 0.2;
Matches 10; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 18 DEPTHLYTLVPRDNTYEVKINSQ 42
DB 181 DKLTHVITALLPDLNRLVDSGE 205

RESULT 12
US-08-906-865-3
Sequence 3, Application US/08906865
Patent No. 6043168
GENERAL INFORMATION:
APPLICANT: Greengard, Paul
APPLICANT: Porton, Barbara
APPLICANT: Kao, Hung-Teh
TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,865
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 582 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

DESCRIPTION: /desc = "Synapsin Ila"
HYPOTHEtical: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-906-865-3

Query Match 23.8%; Score 61.5; DB 3; Length 582;
Best Local Similarity 40.0%; Pred. No. 1.9;
Matches 14; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

QY 2 YKGNVLINKDIRCKDDETHLYTLVPRDNTYEV 36
DB 130 FRGKKVLGDYDIKVEQAEFSEL-NLVAHADGTYAV 163

RESULT 13
US-09-129-668-3
Sequence 3, Application US/09129668B
Patent No. 6429010
GENERAL INFORMATION:
APPLICANT: Greengard, Paul
APPLICANT: Porton, Barbara
APPLICANT: Kao, Hung-Teh
TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 600-1-202 CIP
CURRENT APPLICATION NUMBER: US/09/129,668B
CURRENT FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 08/906,865
EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 3
LENGTH: 582
TYPE: PRT
ORGANISM: Homo sapiens
US-09-129-668-3

Query Match 23.8%; Score 61.5; DB 4; Length 582;
Best Local Similarity 40.0%; Pred. No. 1.9;
Matches 14; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

QY 2 YKGNVLINKDIRCKDDETHLYTLVPRDNTYEV 36
DB 130 FRGKKVLGDYDIKVEQAEFSEL-NLVAHADGTYAV 163

RESULT 14
US-09-252-991A-18861
Sequence 18861, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18861
LENGTH: 588
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18861

Query Match 21.3%; Score 55; DB 4; Length 588;
Best Local Similarity 48.0%; Pred. No. 17;
Matches 12; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Search completed: October 4, 2004, 13:07:20
Job time : 10.9529 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2004, 13:06:03 ; Search time 36.0294 Seconds
(without alignments)
437.647 Million cell updates/sec

Title: US-09-807-148-6

Perfect score: 258

Sequence: 1 NYKGNVLINKDKKDEP.....PDNTYEVKIDNSQVSGSLE 49

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	258	100.0	61	10	US-09-828-000-8
2	258	100.0	61	15	US-10-405-588-8
3	258	100.0	180	10	US-09-828-000-3
4	258	100.0	180	15	US-10-405-588-3
5	258	100.0	416	10	US-09-828-000-2
6	258	100.0	416	14	US-10-316-253-2
7	258	100.0	416	14	US-10-316-253-4
8	258	100.0	416	15	US-10-316-253-6
9	258	100.0	416	15	US-10-405-588-2
10	258	100.0	417	10	US-09-906-392A-36
11	258	100.0	417	14	US-10-161-359-29
12	258	100.0	417	15	US-10-367-093-14
13	179	69.4	395	15	US-10-369-493-6343
14	175	67.8	35	10	US-09-828-000-7
15	175	67.8	35	15	US-10-405-588-7

16 175 67.8 61 10 US-09-828-000-4
17 175 67.8 61 15 US-10-405-588-4
18 171 66.3 94 14 US-10-029-386-32394
19 163 63.2 210 16 US-10-767-701-55877
20 148 57.4 268 12 US-10-425-114-38848
21 148 57.4 346 12 US-10-425-114-48930
22 148 57.4 421 16 US-10-767-701-46544
23 148 57.4 435 12 US-10-425-114-70304
24 147 57.0 442 16 US-10-437-963-114914
25 147 57.0 667 16 US-10-437-963-114860
26 146 56.6 388 12 US-10-425-114-46405
27 146 56.6 391 12 US-10-425-114-69519
28 146 56.6 442 12 US-10-425-114-46869
29 145 56.2 390 15 US-10-161-927-46
30 142 55.0 420 9 US-09-844-006A-2
31 142 55.0 425 16 US-10-437-963-122222
32 140 54.3 290 12 US-10-425-114-44768
33 140 54.3 422 12 US-10-424-598-277445
34 140 54.3 422 16 US-10-767-701-45264
35 139 53.9 434 12 US-10-425-114-70140
36 139 53.9 439 12 US-10-425-114-65495
37 138 53.5 247 12 US-10-424-599-153809
38 138 53.5 372 12 US-10-425-114-44621
39 138 53.5 372 12 US-10-425-114-54997
40 138 53.5 418 12 US-10-424-599-153808
41 137 53.1 391 12 US-10-424-599-190956
42 137 53.1 391 12 US-10-425-114-46228
43 137 53.1 391 12 US-10-425-114-55995
44 137 53.1 420 12 US-10-424-599-190958
45 137 53.1 434 12 US-10-425-114-57598

ALIGNMENTS

RESULT 1

US-09-828-000-8
; Sequence 8, Application US/09828000
; Publication No. US20030078198A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 8
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Fragment 5
US-09-828-000-8

Query Match 100.0%; Score 258; DB 10; Length 61;
Best Local Similarity 100.0%; Pred. No. 2.3e-27;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDKKDEPHTLYTLVIRPDNTYEVKIDNSQVSGSLE 49
DB 13 NYKGNVLINKDKKDEPHTLYTLVIRPDNTYEVKIDNSQVSGSLE 61

RESULT 2

US-10-405-588-8
; Sequence 8, Application US/10405588
; Publication No. US20030216299A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/10/405,588
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US/09/828,000

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; PRIOR FILING DATE: 2001-04-06
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Fragment 5
US-10-405-588-8

Query Match      100.0%; Score 258; DB 15; Length 61;
Best Local Similarity 100.0%; Pred. No. 2.3e-27;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYGKNVLINKIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSLE 49
Db 13 NYGKNVLINKIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSLE 61

RESULT 3
US-09-828-000-3
; Sequence 3, Application US/09828000
; Publication No. US20030078198A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Vasostatin
US-09-828-000-3

Query Match      100.0%; Score 258; DB 10; Length 180;
Best Local Similarity 100.0%; Pred. No. 8.9e-27;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYGKNVLINKIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSLE 49
Db 132 NYGKNVLINKIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSLE 180

RESULT 4
US-10-405-588-3
; Sequence 3, Application US/10405588
; Publication No. US20030216299A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/10/405,588
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US/09/828,000
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Vasostatin
US-10-405-588-3

Query Match      100.0%; Score 258; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 8.9e-27;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYGKNVLINKIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSLE 49
Db 132 NYGKNVLINKIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSLE 180
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RESULT 5
US-09-828-000-2
; Sequence 2, Application US/09828000
; Publication No. US20030078198A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Calreticulin
US-09-828-000-2

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Best Local Similarity 100.0%; Pred. No. 2.5e-26;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYGKNVLINKIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSLE 49
Db 149 NYGKNVLINKIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSLE 197

RESULT 6
US-10-316-253-2
; Sequence 2, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-2

Query Match      100.0%; Score 258; DB 14; Length 416;
Best Local Similarity 100.0%; Pred. No. 2.5e-26;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYGKNVLINKIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSLE 49
Db 149 NYGKNVLINKIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSLE 197

RESULT 7
US-10-316-253-4
; Sequence 4, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
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; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Rattus norvegicus.
US-10-316-253-4

Query Match 100.0%; Score 258; DB 14; Length 416;
Best Local Similarity 100.0%; Pred. No. 2.5e-26;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NYGKNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 49
Db 149 NYGKNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 8
US-10-316-253-6
; Sequence 6, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Thompson, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-6

Query Match 100.0%; Score 258; DB 14; Length 416;
Best Local Similarity 100.0%; Pred. No. 2.5e-26;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NYGKNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 49
Db 149 NYGKNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 9
US-10-405-588-2
; Sequence 2, Application US/10405588
; Publication No. US20030216299A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/10/405,588
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US/09/828,000
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Calreticulin
US-10-405-588-2

Query Match 100.0%; Score 258; DB 15; Length 416;
Best Local Similarity 100.0%; Pred. No. 2.5e-26;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NYGKNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 49
Db 149 NYGKNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 10
US-09-906-393A-36
; Sequence 36, Application US/09906393A
; Publication No. US2003009970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-393A-36

Query Match 100.0%; Score 258; DB 10; Length 417;
Best Local Similarity 100.0%; Pred. No. 2.5e-26;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 149 NYGKNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 11
US-10-161-959-29
; Sequence 29, Application US/10161959
; Publication No. US20030096748A1
; GENERAL INFORMATION:
; APPLICANT: Holosnitz, Joseph
; APPLICANT: Ling, Song
; TITLE OF INVENTION: Methods and Compositions for the Treatment of Diseases Associated with Signal Transduction Aberrations
; FILE REFERENCE: UM-07135
; CURRENT APPLICATION NUMBER: US/10/161,959
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/295,691
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-161-959-29

Query Match 100.0%; Score 258; DB 14; Length 417;
Best Local Similarity 100.0%; Pred. No. 2.5e-26;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NYGKNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 49
Db 149 NYGKNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 197

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RESULT 12
US-10-367-093-14
; Sequence 14, Application US/10367093
; Publication No. US20030216315A1
; GENERAL INFORMATION:
; APPLICANT: Duke University
; APPLICANT: Nicchitta, Chris
; APPLICANT: Baker-LePain, Julie
; TITLE OF INVENTION: MODULATION OF IMMUNE RESPONSE BY NON-PEPTIDE BINDING STRESS RESPON
; FILE REFERENCE: 180/145
; CURRENT APPLICATION NUMBER: US/10/367,093
; CURRENT FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-093-14

Query Match          69.4%; Score 179; DB 15; Length 395;
Best Local Similarity 67.3%; Pred. No. 1.2e-15;
Matches 33; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDDEFTHTLYLIVRPDNTYEVKIDNSQVSGSLE 49
Db 149 NYKGNVLINKDIRCKDDEFTHTLYLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 13
US-10-369-493-6343
; Sequence 6343, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6343
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6343

Query Match          69.4%; Score 179; DB 15; Length 395;
Best Local Similarity 67.3%; Pred. No. 1.2e-15;
Matches 33; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDDEFTHTLYLIVRPDNTYEVKIDNSQVSGSLE 49
Db 144 NYKGNVLINKDIRCKDDEFTHTLYLIVRPDNTYEVKIDNSQVSGSLE 192

RESULT 14
US-09-828-000-7
; Sequence 7, Application US/09828000
; Publication No. US20030078198A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
```

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; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Fragment 4
US-09-828-000-7

Query Match          67.8%; Score 175; DB 10; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.1e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDDEFTHTLYLIVRPDN 32
Db 4 NYKGNVLINKDIRCKDDEFTHTLYLIVRPDN 35

RESULT 15
US-10-405-588-7
; Sequence 7, Application US/10405588
; Publication No. US20030216299A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/10/405,588
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US/09/828,000
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Fragment 4
US-10-405-588-7

Query Match          67.8%; Score 175; DB 15; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.1e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDDEFTHTLYLIVRPDN 32
Db 4 NYKGNVLINKDIRCKDDEFTHTLYLIVRPDN 35

Search completed: October 4, 2004, 13:17:33
Job time : 36.0294 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2004, 12:52:12 ; Search time 7.20588 Seconds
(without alignments)
354.077 Million cell updates/sec

Title: US-09-807-148-6
Perfect score: 258
Sequence: 1 NYGKNVLINKDIRCKDEF.....PDNTYEVKIDNSQVESGSL 49

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	258	100.0	416	1	CRTC_MOUSE
2	258	100.0	416	1	CRTC_RAT
3	258	100.0	417	1	CRTC_CRIGR
4	258	100.0	417	1	CRTC_HUMAN
5	258	100.0	418	1	CRTC_RABIT
6	253	98.1	417	1	CRT1_BOVIN
7	253	98.1	421	1	CRT2_BOVIN
8	209	81.0	406	1	CRTC_DROME
9	182	70.5	388	1	RALL_ONCVO
10	182	70.5	393	1	CRTC_SCHMA
11	179	69.4	395	1	CRTC_CABEL
12	164	63.6	420	1	CRTC_CHLRE
13	148.5	57.6	424	1	CRTC_DICDI
14	147	57.0	380	1	CRTC_MOUSE
15	145	56.2	384	1	CRTC_HUMAN
16	145	56.2	421	1	CRTC_PORAR
17	144	55.8	416	1	CRTC_BETVU
18	143	55.4	415	1	CRTC_RICCO
19	143	55.4	424	1	CRTC_MAIZE
20	142	55.0	420	1	CRTC_ARATH
21	138	53.5	425	1	CRT1_ARATH
22	136	52.7	401	1	CRTC_EUGR
23	135	52.3	416	1	CRTC_NICPL
24	134	51.9	424	1	CRTC_ORYSA
25	132	51.2	424	1	CRTC_ARATH
26	128.5	49.8	416	1	CRTC_BERST
27	101	39.1	591	1	CALX_MOUSE
28	101	39.1	591	1	CALX_RAT
29	101	39.1	592	1	CALX_HUMAN
30	100	38.8	593	1	CALX_CANFA
31	95	36.8	610	1	CALG_HUMAN
32	93.5	36.2	611	1	CALG_MOUSE
33	89	34.5	560	1	CALX_SCHPO

34 78 30.2 619 1 CALX_CABEL
35 71 27.5 546 1 CALX_SOYBN
36 68 26.4 530 1 CALX_ARATH
37 68 26.4 540 1 CALX_HELTU
38 64 24.8 540 1 MTAL_ACICA
39 62 24.0 532 1 CAX2_ARATH
40 61.5 23.8 582 1 SYN2_HUMAN
41 60.5 23.4 586 1 SYN2_RAT
42 60 23.3 474 1 LAM3_MOUSE
43 60 23.3 592 1 LAM2_MOUSE
44 58 22.5 763 1 CADQ_MOUSE
45 57 22.1 362 1 YCIS_YEAST

ALIGNMENTS

RESULT 1
CRTC_MOUSE
ID CRTC_MOUSE STANDARD; PRT; 416 AA.
AC P14211;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).
GN CALR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.
RX STRAIN=BALE/C; TISSUE=Liver;
RC MEDLINE=90059955; PubMed=2583110;
RA Smith M.J., Koch G.L.E.;
RT "Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a major calcium binding ER/SR protein.";
RL EMBO J. 8:3581-3586 (1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93013037; PubMed=1398135;
RA Mazzarella R.A., Gold P., Cunningham M., Green M.;
RT "Determination of the sequence of an expressible cDNA clone encoding ERp60/calregulin by the use of a novel nested set method.";
RL Gene 120:217-225 (1992).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=FVB/N-3; TISSUE=Mammary gland;
RC MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley A.C., Touchman J.W., Green E.D., Dickinson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [4]
RP SEQUENCE OF 18-38.
RX TISSUE=Fibroblast;
RC MEDLINE=95009907; PubMed=7523108;

RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 RL using preparative two-dimensional gel electrophoresis.",
 CC Electrophoresis 15:735-745(1994).
 CC -1- FUNCTION: This protein binds calcium. There are both high and
 CC low affinity calcium-binding sites.
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: Belongs to the calreticulin family.
 CC
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 CC
 DR EMBL; X14926; CAA33053.1; -
 DR EMBL; M22988; AAA37569.1; -
 DR EMBL; BC003453; AAH03453.1; -
 DR PIR; S06763; S06763.
 DR SWISS-2DPAGE; P14211; MOUSE.
 DR MGD; MGI:88252; Calr.
 DR GO; GO:0005509; F:calcium ion binding; IDA.
 DR InterPro; IPR009033; Calret_calmex_P.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR008985; ConA-like lec.gl.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PIRSF002356; Calreticulin; 1.
 DR PROSITE; PS00626; CALRETICULIN.
 DR PROSITE; PS001866; Calreticulin; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 416
 FT DOMAIN 18 197
 FT DOMAIN 198 308
 FT DOMAIN 309 416
 FT DOMAIN 191 255
 FT REPEAT 191 202
 FT REPEAT 210 221
 FT REPEAT 227 238
 FT REPEAT 244 255
 FT DOMAIN 259 297
 FT REPEAT 259 269
 FT REPEAT 273 283
 FT REPEAT 287 297
 FT DOMAIN 351 407
 FT DISULFID 137 163
 FT SITE 413 416
 FT SEQUENCE 416 AA; 47994 MW; 24C03B00913408D8 CRC64;
 Query Match 100.0%; Score 258; DB 1; Length 416;
 Best Local Similarity 100.0%; Pred. No. 8.1e-26;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NYKGNVLINKDKCKDEFFHLYTLVPRNTVEYKIDNSQVSGSLE 49
 DB 149 NYKGNVLINKDKCKDEFFHLYTLVPRNTVEYKIDNSQVSGSLE 197
 RESULT 2
 ID_CRTC RAT STANDARD; PRT; 416 AA.
 AC P18418; P18452;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (Erp60) (CALBP)
 DE (Calcium-binding protein 3) (CABP3).
 GN CALR.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_taxID=10116;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain cortex;
 RX MEDLINE=90370496; PubMed=2395661;
 RA Murthy K.K., Banville D., Srikanth C.B., Carrier F., Bell A.,
 RA Holmes C., Patel Y.C.;
 RT "Structural homology between the rat calreticulin gene product and
 RT the Onchocerca volvulus antigen Rai-1.";
 RL Nucleic Acids Res. 18:4933-4933(1990).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=93202172; PubMed=8453984;
 RA Nakamura M., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai K.,
 RA Okinaga S., Kobayashi T.;
 RT "An endoplasmic reticulum protein, calreticulin, is transported into
 RT the acrosome of rat sperm.";
 RL Exp. Cell Res. 205:101-110(1993).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=95181573; PubMed=7876339;
 RA Soennichsen B., Fuellekrug J., van Nguyen P., Diekmann W.,
 RA Robinson D.G., Mieskes G.;
 RT "Retention and retrieval: both mechanisms cooperate to maintain
 RT calreticulin in the endoplasmic reticulum.";
 RL J. Cell Sci. 107:2705-2717(1994).
 RN [4]
 RN SEQUENCE OF 270-358 FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX Lone Y.C., Bailly A., Latruffe N.;
 RL Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RN SEQUENCE OF 18-29.
 RX MEDLINE=91054414; PubMed=2241926;
 RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
 RA MacLennan D.H., Meldolesi J., Pozzan T.;
 RT "Calreticulin is a candidate for a calsequestrin-like function in
 RT Ca2(+)-storage compartments (calciosomes) of liver and brain.";
 RL Biochem. J. 271:473-480(1990).
 RN [6]
 RN SEQUENCE OF 18-32.
 RC STRAIN=Sprague-Dawley; TISSUE=Testis;
 RX MEDLINE=92360010; PubMed=1497855;
 RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;
 RT "Calreticulin is present in the acrosome of spermatids of rat
 RT testis.";
 RL Biochem. Biophys. Res. Commun. 186:668-673(1992).
 RN [7]
 RN SEQUENCE OF 18-32.
 RC STRAIN=LEC; TISSUE=Liver;
 RX MEDLINE=94072621; PubMed=8251535;
 RA Yokoi T., Nagayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,
 RA Kamataki T.;
 RT "Identification of protein disulfide isomerase and calreticulin as
 RT autoimmune antigens in LEC strain of rats.";
 RL Biochim. Biophys. Acta 1158:339-344(1993).
 CC -1- FUNCTION: This protein binds calcium. There are both high and low
 CC affinity calcium-binding sites.
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: Belongs to the calreticulin family.
 CC -1- CAUTION: Was originally (Ref.2) thought to be D-beta-
 CC hydroxybutyrate dehydrogenase.
 CC
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CC EMBL; D78308; BA01345.1; -
 CC EMBL; X53363; CAA37446.1; -
 CC EMBL; X13702; CAA31987.1; ALT_SEQ.
 CC EMBL; X79327; CAA55890.1; -
 CC FIR; JH0819; JH0819.
 CC PDB; 1LHN; 26-FEB-02.
 CC PDB; 1K91; 12-OCT-02.
 CC PDB; 1K9C; 12-OCT-02.

CC InterPro; IPR009033; Calret calnex P.
 CC InterPro; IPR001580; Calreticulin.
 CC InterPro; IPR008985; ConA like lec gl.
 CC InterPro; IPR000886; ER target S.
 CC Pfam; PF00262; calreticulin; 1.
 CC PIRSF; PIRSF002356; Calreticulin; 1.
 CC PRINTS; PR00626; CALRETICULIN.
 CC ProDom; PD001866; Calreticulin; 1.
 CC PROSITE; PS0014; ER TARGET; 1.
 CC PROSITE; PS00803; CALRETICULIN; 1.
 CC PROSITE; PS00804; CALRETICULIN; 2; 1.
 CC PROSITE; PS00805; CALRETICULIN REPEAT; 3.
 CC Endoplasmic reticulum; Calcium-binding; Repeat; Signal; 3D-structure.

FT SIGNAL 1 17
 FT CHAIN 18 416 CALRETICULIN.
 FT DOMAIN 18 197 N-DOMAIN.
 FT DOMAIN 198 308 P-DOMAIN.
 FT DOMAIN 309 416 C-DOMAIN.
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
 FT REPEAT 191 202 1-1.
 FT REPEAT 210 221 1-2.
 FT REPEAT 227 238 1-3.
 FT REPEAT 244 255 1-4.
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
 FT REPEAT 273 283 2-1.
 FT REPEAT 287 297 2-2.
 FT REPEAT 351 407 ASP/GLU/LYS-RICH.
 FT DOMAIN 137 163 BY SIMILARITY.
 FT DISULFID 137 163
 FT SITE 413 416 PREVENT SECRETION FROM ER.
 FT SEQUENCE 416 AA; 47995 MW; 26713CED31A2970 CRC64;

Query Match 100.0%; Score 258; DB 1; Length 416;
 Best Local Similarity 100.0%; Pred. No. 8.1e-26;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDDEFTHTLVLPDNTYEVKIDNSQVSGSLE 49
 DB 149 NYKGNVLINKDIRCKDDEFTHTLVLPDNTYEVKIDNSQVSGSLE 197

RESULT 3

ID CRIC CRIGR STANDARD; PRT; 417 AA.
 AC Q8KJH7;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).
 GN CALR.
 OS Cricetus griseus (Chinese hamster).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Cricetinae;
 OC Cricetulus.
 OX NCBI_TaxID=10029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chung J.Y., Lee G.M.;

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 CC !- FUNCTION: This protein binds calcium. There are both high and low
 CC affinity calcium-binding sites.
 CC !- SUBUNIT: Monomer.
 CC !- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC !- SIMILARITY: Belongs to the calreticulin family.

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CC EMBL; AY100688; AAM48568.1; -
 CC InterPro; IPR009033; Calret calnex P.
 CC InterPro; IPR001580; Calreticulin.
 CC InterPro; IPR008985; ConA like lec gl.
 CC InterPro; IPR000886; ER target S.
 CC Pfam; PF00262; calreticulin; 1.
 CC PIRSF; PIRSF002356; Calreticulin; 1.
 CC PRINTS; PR00626; CALRETICULIN.
 CC ProDom; PD001866; Calreticulin; 1.
 CC PROSITE; PS00803; CALRETICULIN; 1.
 CC PROSITE; PS00804; CALRETICULIN; 2; 1.
 CC PROSITE; PS00805; CALRETICULIN REPEAT; 3.
 CC Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein; Signal.

FT SIGNAL 1 17
 FT CHAIN 18 417 CALRETICULIN.
 FT DOMAIN 18 197 N-DOMAIN.
 FT DOMAIN 198 308 P-DOMAIN.
 FT DOMAIN 309 417 C-DOMAIN.
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
 FT REPEAT 191 202 1-1.
 FT REPEAT 210 221 1-2.
 FT REPEAT 227 238 1-3.
 FT REPEAT 244 255 1-4.
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
 FT REPEAT 273 283 2-1.
 FT REPEAT 287 297 2-2.
 FT REPEAT 351 407 ASP/GLU/LYS-RICH.
 FT DOMAIN 137 163 BY SIMILARITY.
 FT DISULFID 137 163
 FT SITE 414 417 PREVENT SECRETION FROM ER (POTENTIAL).
 FT SEQUENCE 417 AA; 48242 MW; D617DA37D14F2D45 CRC64;

Query Match 100.0%; Score 258; DB 1; Length 417;
 Best Local Similarity 100.0%; Pred. No. 8.2e-26;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDDEFTHTLVLPDNTYEVKIDNSQVSGSLE 49
 DB 149 NYKGNVLINKDIRCKDDEFTHTLVLPDNTYEVKIDNSQVSGSLE 197

RESULT 4

ID CRIC HUMAN STANDARD; PRT; 417 AA.
 AC P27797;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).
 GN CALR OR CRIC
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92013129; PubMed=1919005;

TISSUE=Liver;
MEDLINE=931162045; PubMed=1286669;
Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargis R.,
Appel R.D., Hughes G.J.;
"Human liver protein map: a reference database established by
microsequencing and gel comparison";
Electrophoresis 13:992-1001(1992).
[10]
PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.
TISSUE=Xeratinocytes;
MEDLINE=93162043; PubMed=1286667;
Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
Vandekerckhove J.;
"Microsequences of 145 proteins recorded in the two-dimensional gel
protein database of normal human epidermal keratinocytes.";
Electrophoresis 13:960-969(1992).
[11]
SEQUENCE OF 18-26.
TISSUE=Colon carcinoma;
MEDLINE=97295308; PubMed=9150948;
Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
"A two-dimensional gel database of human colon carcinoma proteins.";
Electrophoresis 18:605-613(1997).
-!- FUNCTION: This protein binds calcium. There are both high and low
affinity calcium-binding sites.
-!- SUBUNIT: Monomer (by similarity).
-!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
-!- SIMILILARITY: Belongs to the calreticulin family.
-!- CAUTION: Was originally (Ref.2) thought to be the 52 kDa Ro
autoantigen.

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EMBL; M84739; AAAS1916.1; -;
EMBL; M32294; AAA36582.1; -;
EMBL; AY047586; AAL13126.1; -;
EMBL; AD000092; AAB51176.1; -;
EMBL; BC002500; AAH02500.1; -;
EMBL; BC007911; AAH07911.1; -;
EMBL; BC020493; AAH20493.1; -;
PIR; A42330; A37047.
PDB; 2CLR; 3I-MAR-95.
SWISS-2DPAGE; P27797; HUMAN.
Aarhus/Ghent-2DPAGE; 9401; IEF.
HSC-2DPAGE; P27797; HUMAN.
PHCI-2DPAGE; P27797; -;
PMWA-2DPAGE; P27797; -;
Sienna-2DPAGE; P27797; -;
GeneW; HGNC:1455; CALR.
MIM; 103091; -;
GO; GO:0006355; P:regulation of transcription, DNA-dependent; TAS.
InterPro; IPRO09033; Calret calnex P.
InterPro; IPRO01580; Calreticulin.
InterPro; IPRO08985; ConA-like lec_gl.
Pfam; PF00262; calreticulin; 1.
PIRSP; PIRSF002356; Calreticulin; 1.
PRINTS; PR00626; CALRETICULIN.
ProDom; PD001866; Calreticulin; 1.
PROSITE; PS00014; ER_TARGET; 1.
PROSITE; PS00803; CALRETICULIN_1; 1.
PROSITE; PS00804; CALRETICULIN_2; 1.
PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
Endoplasmic reticulum; Calcium-binding; Repeat; Signal; 3D-structure.
1 17
CHAIN 18 417 CALRETICULIN

```
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 417 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 414 417 PREVENT SECRETION FROM ER.
FT CONFLICT 35 35 MISSING (IN REF. 3).
SQ SEQUENCE 417 AA; 48141 MW; BC37C3COF1054FB2 CRC64;

Query Match 100.0%; Score 258; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 8.2e-26; Indels 0; Gaps 0;
Matches 49; Conservative 0; Mismatches 0;

QY 1 NYKGNVINKDIRCKDDETHLYTLIVRPDNTYEVKIDNSQVSGSLE 49
Db 149 NYKGNVINKDIRCKDDETHLYTLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 5
CRIC RABIT STANDARD; PRT; 418 AA.
AC P15253;

DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).
GN CALR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;

[1]
RN RN SEQUENCE FROM N.A.
RP TISSUE=Slow-twitch skeletal muscle;
RX MEDLINE=90094320; PubMed=2600080;
RA Fliegel L., Burns K., MacLennan D.H., Reithmeier R.A.F., Michalak M.;
RT "Molecular cloning of the high affinity calcium-binding protein
(calsarcoplasmic reticulum) of skeletal muscle sarcoplasmic reticulum.";
RL J. Biol. Chem. 264:21522-21528(1989).

[2]
RN RN SEQUENCE FROM N.A.
RP TISSUE=Fast-twitch skeletal muscle;
RX MEDLINE=91282795; PubMed=2059224;
RA Fliegel L., Michalak M.;
RT "Fast-twitch and slow-twitch skeletal muscles express the same
isoform of calreticulin.";
RL Biochem. Biophys. Res. Commun. 177:979-984(1991).

[3]
RN RN SEQUENCE OF 18-36.
RX MEDLINE=91054414; PubMed=2241926;
RA Treves S., de Mattei M., Ianfredi M., Villa A., Green N.M.,
RA MacLennan D.H., Meldolesi J., Pozzan T.;
RT "Calreticulin is a candidate for a calsequestrin-like function in
Ca2(+)-storage compartments (calciosomes) of liver and brain.";
RL Biochem. J. 271:473-480(1990).

[4]
RN RN SEQUENCE OF 18-46.
RX MEDLINE=9201375; PubMed=2016321;
RA Milner R.E., Bakes S., Shemanko C., Carpenter M.R., Smillie L.,
RA Vance J.E., Opas M., Michalak M.;
RT "Calreticulin, and not calsequestrin, is the major calcium binding
protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic
reticulum.";
RL J. Biol. Chem. 266:7155-7165(1991).
```

DT 01-OCT-1996 (Rel. 34, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Calreticulin, brain isoform 1 precursor (CRP55) (Calregulin) (HACBP).
 GN CALR OR CRT.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Hossain M.A., Takuwa K., Minakata H., Nakajima T.;
 RT "Bovine brain calreticulin."
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 18-417.
 RC TISSUE=Brain;
 RX MEDLINE=94183174; PubMed=8135753;
 RA Matsuo K., Seta K., Yamakawa Y., Okuyama T., Shinoda T., Isobe T.;
 RT "Covalent structure of bovine brain calreticulin."
 RL Biochem. J. 298:435-442(1994).
 CC -!- FUNCTION: This protein binds calcium. There are both high and low
 CC affinity calcium-binding sites.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -!- SIMILARITY: Belongs to the calreticulin family.
 CC
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 CC
 CC EMBL; AB067687; BAB86913.1;
 DR InterPro; IPR009033; Calret calnex P.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR008985; ConA-like lec_gl.
 DR InterPro; IPR000886; ER target S.
 DR Pfam; PF00262; calreticulin; 1.
 DR Pfam; PF00262; calreticulin; 1.
 DR PIRSF; PIRSF002356; Calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN 1; 1.
 DR PROSITE; PS00804; CALRETICULIN 2; 1.
 DR PROSITE; PS00805; CALRETICULIN REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 417 CALRETICULIN, BRAIN ISOFORM 1.
 FT DOMAIN 18 197 N-DOMAIN.
 FT DOMAIN 198 308 P-DOMAIN.
 FT DOMAIN 309 417 C-DOMAIN.
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
 FT REPEAT 191 202 1-1.
 FT REPEAT 210 221 1-2.
 FT REPEAT 227 238 1-3.
 FT REPEAT 244 255 1-4.
 FT REPEAT 259 297 3 X APPROXIMATE REPEATS.
 FT REPEAT 259 269 2-1.
 FT REPEAT 273 283 2-2.
 FT REPEAT 287 297 2-3.
 FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
 FT DISULFID 137 163 N-LINKED (GLCNAC...).
 FT CARBOHYD 179 179 PRESENT SECRETION FROM ER (POTENTIAL).
 FT SITE 414 417
 SQ SEQUENCE 417 AA; 48038 MW; 7BF812C/B5417B59 CRC64;
 Query Match 98.1%; Score 253; DB 1; Length 417;
 Best Local Similarity 98.0%; Pred. No. 3.6e-25;

Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NYKGNVLINLKIRCKDETHLYTLVRPDNTYEVKIDNSQVSGSLE 49
 DB 149 NYKGNVLINLKIRCKDETHLYTLVRPDNTYEVKIDNSQVSGSLE 197
 RESULT 7
 CRT2_BOVIN
 ID CRT2_BOVIN STANDARD; PRT; 421 AA.
 AC P42918;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Calreticulin, brain isoform 2 precursor (CRP55) (Calregulin) (HACBP).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93385184; PubMed=8373827;
 RA Liu N., Fine R.B., Johnson R.J.;
 RT "Comparison of cDNAs from bovine brain coding for two isoforms of
 RT calreticulin."
 RL Biochim. Biophys. Acta 1202:70-76(1993).
 CC -!- FUNCTION: This protein binds calcium. There are both high and low
 CC affinity calcium-binding sites.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -!- SIMILARITY: Belongs to the calreticulin family.
 CC
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 CC
 CC EMBL; L13462; AAC37307.1;
 DR PIR; S36799; S36799.
 DR InterPro; IPR009033; Calret calnex P.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR008985; ConA-like lec_gl.
 DR InterPro; IPR000886; ER target S.
 DR Pfam; PF00262; calreticulin; 1.
 DR PIRSF; PIRSF002356; Calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN 1; 1.
 DR PROSITE; PS00804; CALRETICULIN 2; 1.
 DR PROSITE; PS00805; CALRETICULIN REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 34 POTENTIAL.
 FT CHAIN 35 421 CALRETICULIN, BRAIN ISOFORM 2.
 FT DOMAIN 35 201 N-DOMAIN.
 FT DOMAIN 202 312 P-DOMAIN.
 FT DOMAIN 313 421 C-DOMAIN.
 FT DOMAIN 195 259 4 X APPROXIMATE REPEATS.
 FT REPEAT 195 206 1-1.
 FT REPEAT 214 225 1-2.
 FT REPEAT 231 242 1-3.
 FT REPEAT 248 259 1-4.
 FT DOMAIN 263 301 3 X APPROXIMATE REPEATS.
 FT REPEAT 263 273 2-1.
 FT REPEAT 277 287 2-2.
 FT REPEAT 291 301 2-3.
 FT DOMAIN 366 411 ASP/GLU/LYS-RICH.
 FT DISULFID 141 167 BY SIMILARITY.

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FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 418 421 PREVENT SECRETION FROM ER.
SQ SEQUENCE 421 AA; 48812 MW; 0257E959F71528BC CRC64;

Query Match
Best Local Similarity 98.1%; Score 253; DB 1; Length 421;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDRCKDETHLYTLVRPNTYEVKIDNSQVSGSLE 49
Db 153 NYKGNVLINKDRCKDETHLYTLVRPNTYEVKIDNSQVSGSLE 201

RESULT 8
CRIC DROME STANDARD; PRT; 406 AA.
AC P29413; Q9VHA3;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP).
GN CRC OR CG9429.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN RN
RP SEQUENCE FROM N.A.
RX MEDLINE=93208374; PubMed=1296819;
RA Smith M.J.;
RT "Nucleotide sequence of a Drosophila melanogaster gene encoding a
RT calreticulin homologue."
RL DNA Seq. 3:247-250(1992).
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D.; Celnik S.E.; Holt R.A.; Evans C.A.; Gocayne J.D.;
RA Amanatides P.G.; Scher S.E.; Li P.W.; Hoskins R.A.; Galle R.F.;
RA George R.A.; Lewis S.E.; Richards S.; Ashburner M.; Henderson S.N.;
RA Sutton G.G.; Wortman J.R.; Vandell M.D.; Zhang Q.; Chen L.X.;
RA Brandon R.C.; Rogers J.-H.C.; Blazey R.G.; Champagne M.; Pfeiffer B.D.;
RA Wan K.H.; Doyle C.; Baxter E.G.; Helt G.; Nelson C.R.; Miklos G.L.G.;
RA Abril J.F.; Agbayani A.; An H.-J.; Andrews-pfankoch C.; Baldwin D.;
RA Balow R.M.; Basu A.; Baxendale J.; Bayraktaroglu L.; Beasley E.M.;
RA Beeson K.Y.; Benos P.V.; Herman B.P.; Bhandari D.; Bolshakov S.;
RA Borkova D.; Botchan M.R.; Bouck J.; Brokstein P.; Brottier P.;
RA Burtis K.C.; Buesam D.A.; Butler H.; Cadieu E.; Center A.; Chandra I.;
RA Cherry J.M.; Cawley S.; Dahlke C.; Davenport L.B.; Davies P.;
RA de Pablo B.; Delcher A.; Deng Z.; Mays A.D.; Dew I.; Dietz S.M.;
RA Dodson K.; Doup L.E.; Downes M.; Dugan-Rocha S.; Dunkov B.C.; Dunn P.;
RA Durbin K.J.; Evangelista C.C.; Ferraz C.; Ferreira S.; Fleischmann W.;
RA Foeller C.; Gabriellian A.E.; Garg N.S.; Gelbart W.M.; Glasser K.;
RA Glodek A.; Gong F.; Gorrell J.H.; Gu Z.; Guan P.; Harris M.;
RA Harris N.L.; Harvey D.A.; Heiman T.J.; Hernandez J.R.; Houck J.;
RA Hostin D.; Houston K.A.; Howland T.J.; Wei M.-H.; Ibegwam C.;
RA Jalali M.; Kalush F.; Karpen G.H.; Ke Z.; Kennison J.A.; Ketchum K.A.;
RA Kimmel B.E.; Kodira C.D.; Kraft C.; Kravitz S.; Kulp D.; Lai Z.;
RA Laslo P.; Lei Y.; Levitsky A.; Li J.H.; Li Z.; Liang Y.; Lin X.;
RA Liu X.; Mattei B.; McIntosh T.C.; McLeod M.P.; McPherson D.;
RA Merkulov G.; Milshina N.V.; Mobarry C.; Morris J.; Moshrefi A.;
RA Mount S.M.; Moy M.; Murphy L.; Muzny D.M.; Nelson D.L.;
RA Nelson D.R.; Nelson K.A.; Nixon K.; Nusken D.R.; Pacle J.M.;
RA Palazzolo M.; Pittman G.S.; Pan S.; Pollard J.; Puri V.; Reese M.G.;
RA Reinert K.; Remington K.; Saunders R.D.C.; Scheeler F.; Shen H.;
RA Shue B.C.; Sigen-Kiamos I.; Simpson M.; Skupski M.P.; Smith T.;
RA Spier E.; Spradling A.C.; Stapleton M.; Strong R.; Sun E.;
RA Svitksas R.; Tector C.; Turner R.; Venter E.; Wang A.H.; Wang X.;
RA Wang Z.-Y.; Wassarman D.A.; Weinstock G.M.; Weissbach J.;
RA Williams S.M.; Woodage T.; Worley K.C.; Wu D.; Yang S.; Yao Q.A.;
RA Ye J.; Yeh R.-F.; Zaveri J.S.; Zhan M.; Zhang G.; Zhao Q.; Zheng L.;
RA Zheng X.H.; Zhong F.N.; Zhong W.; Zhou X.; Zhu S.; Zhu X.; Smith H.O.

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RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN RN
RP SEQUENCE OF 91-124 AND 182-220.
RX MEDLINE=90307991; PubMed=2365822;
RA McCaulliffe D.P., Zappi E., Lieu T.S., Michalak M., Sontheimer R.D.,
RA Capra J.D.;
RT "A human Ro/SS-A autoantigen is the homologue of calreticulin and is
RT highly homologous with oncohercal RAL-1 antigen and an aplasia
RT 'memory molecule'."
RL J. Clin. Invest. 86:332-335(1990).
CC -!- FUNCTION: This protein binds calcium. There are both high and low
CC affinity calcium-binding sites.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: Belongs to the calreticulin family.
CC
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CC
CC EMBL: X64461; CAA45791.1; -
CC EMBL: AE003683; AAF54416.1; -
CC F1R; A56637; A56637.
CC FlyBase; FBgn005585; Crc.
CC GO; GO:007417; P:central nervous system development; IMP.
CC InterPro; IPR009033; Calret calnex P.
CC InterPro; IPR001580; Calreticulin.
CC InterPro; IPR008985; Cona like lec_gl.
CC InterPro; IPR000886; ER_target_S.
CC Pfam; PF00262; calreticulin; 1.
CC PIRSF; PIRSF002356; Calreticulin; 1.
CC PRINTS; PR00626; CALRETICULIN.
CC ProDom; PD001866; Calreticulin; 1.
CC PROSITE; PS00014; ER_TARGET; 1.
CC PROSITE; PS00803; CALRETICULIN_1; 1.
CC PROSITE; PS00804; CALRETICULIN_2; 1.
CC PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
CC Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 406 CALRETICULIN.
FT CONFLICT 107 107 G -> A (IN REF. 3).
FT CONFLICT 184 184 V -> L (IN REF. 3).
SQ SEQUENCE 406 AA; 46808 MW; 65D72C69D0BEC427 CRC64;

Query Match
Best Local Similarity 81.0%; Score 209; DB 1; Length 406;
Matches 39; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDRCKDETHLYTLVRPNTYEVKIDNSQVSGSLE 49
Db 149 SYKGNVLINKDRCKDDVYTHFTYTLVRPNTYEVLDNKEVSGNLE 197

RESULT 9
RAL1 ONCVO STANDARD; PRT; 388 AA.
ID RAL1 ONCVO
AC P11012;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE RAL-1 protein precursor (41 kDa larval antigen).
GN RAL1
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN RN
RP SEQUENCE FROM N.A.

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CRTC_CABEL
ID CRTC_CABEL STANDARD; PRT; 395 AA.
AC P27798;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Calreticulin precursor.
GN CRT-1 OR Y38A10A.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=92329978; PubMed=1627827;
RA Smith M.J.;
RT "A C. elegans gene encodes a protein homologous to mammalian
  calreticulin."
RL DNA Seq. 2:235-240(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Bauer C., Courtney L., LaPlant Y.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP REVISIONS.
RA Waterston R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: This protein binds calcium. There are both high and low
  affinity calcium-binding sites.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: Belongs to the calreticulin family.
CC
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  or send an email to license@isb-sib.ch).
CC
CC EMBL; X59589; CAA42159.1; -.
CC EMBL; AF125963; AAD14746.1; -.
CC PIR; S25851; S25851.
CC WormPep; Y38A10A.5; CE21562.
CC InterPro; IPR003033; Calret calnex_P.
CC InterPro; IPR001580; Calreticulin.
CC InterPro; IPR008985; ConA-like lec_gl.
CC InterPro; IPR000886; ER_target_S.
CC Pfam; PF00262; calreticulin; 1.
CC PIRSF; PIRSF002356; Calreticulin; 1.
CC PRINTS; PR00626; CALRETICULIN.
CC ProDom; PD001866; Calreticulin; 1.
CC PROSITE; PS00014; ER_TARGET; 1.
CC PROSITE; PS00803; CALRETICULIN_1; 1.
CC PROSITE; PS00804; CALRETICULIN_2; 1.
CC PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
CC PROSITE; PS00805; CALRETICULIN_REPEAT; 1.
CC Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
CC SIGNAL 1 15 POTENTIAL.
CC CHAIN 16 395 CALRETICULIN.
CC DOMAIN ? 192 N-DOMAIN.
CC DOMAIN 193 301 P-DOMAIN.
CC DOMAIN 302 395 C-DOMAIN.
CC FT DOMAIN 186 250 4 X APPROXIMATE REPEATS.
CC FT REPEAT 186 197 1-1.
CC FT REPEAT 205 216 1-2.
CC FT REPEAT 222 233 1-3.
CC FT REPEAT 239 250 1-4.
CC FT REPEAT 254 292 3 X APPROXIMATE REPEATS.
CC FT DOMAIN 254 264 2-1.
CC FT REPEAT 254 264 2-1.
CC FT REPEAT 268 278 2-2.
CC FT REPEAT 282 292 2-3.

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FT DOMAIN 332 390 ASP/GLU/LYS-RICH.
FT DISULFID 133 158 BY SIMILARITY.
FT SITE 392 395 PREVENT SECRETION FROM ER.
SQ SEQUENCE 395 AA; 45616 MW; 35CA7D2EC1D56B03 CRC64;

Query Match 69.4%; Score 179; DB 1; Length 395;
Best Local Similarity 67.3%; Pred. No. 1.3e-15;
Matches 33; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDETHLYTLVRPNTYEVKIDNSQVESGSL 49
  |||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 144 NYKGNLKIKEITCKSDTHLYTLINSDNTYEVKIDGESAQIGSL 192

RESULT 12
CRTC_CHLRE STANDARD; PRT; 420 AA.
ID CRTC_CHLRE
AC Q9STD3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calreticulin precursor.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=137c / CC-125;
RA Zuppin A., Kaydamov C.;
RT "Cloning and characterization of a cDNA encoding Chlamydomonas
  reinhardtii calreticulin."
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: This protein binds calcium. There are both high and low
  affinity calcium-binding sites (By similarity).
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
CC -!- SIMILARITY: Belongs to the calreticulin family.
CC
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  or send an email to license@isb-sib.ch).
CC
CC EMBL; AJ000765; CAB54526.1; -.
CC InterPro; IPR009033; Calret calnex_P.
CC InterPro; IPR001580; Calreticulin.
CC InterPro; IPR008985; ConA-like lec_gl.
CC InterPro; IPR000886; ER_target_S.
CC Pfam; PF00262; calreticulin; 1.
CC PIRSF; PIRSF002356; Calreticulin; 1.
CC PRINTS; PR00626; CALRETICULIN.
CC ProDom; PD001866; Calreticulin; 1.
CC PROSITE; PS00014; ER_TARGET; 1.
CC PROSITE; PS00803; CALRETICULIN_1; 1.
CC PROSITE; PS00804; CALRETICULIN_2; 1.
CC PROSITE; PS00805; CALRETICULIN_REPEAT; 1.
CC Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
CC SIGNAL 1 18 POTENTIAL.
CC CHAIN 19 420 CALRETICULIN.
CC SITE 417 420 PREVENT SECRETION FROM ER (POTENTIAL).
CC SEQUENCE 420 AA; 47327 MW; DD3BA3AFBFB61C9B CRC64;

Query Match 63.6%; Score 164; DB 1; Length 420;
Best Local Similarity 61.7%; Pred. No. 1.2e-13;
Matches 29; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 2 YKGNVLINKDIRCKDETHLYTLVRPNTYEVKIDNSQVESGSL 48
  |||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 153 YKGNVLIKDIAETDQTLVYTLVVKPDNTYQVLDLKEVASGSL 199

```

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RESULT 13
CRTC_DICDI STANDARD; PRT; 424 AA.
AC Q3858;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Calreticulin precursor.
GN CRTC.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RC STRAIN=AX3;
RA Mueller-Taubenberger A., Gerisch G.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: This protein binds calcium. There are both high and low
CC affinity calcium-binding sites (By similarity).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: Belongs to the calreticulin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DE EMBL: U36937; AAB87719.1;
DR DictyBase; DB0001623; CttA.
DR InterPro; IPR009033; Calret_calmex_P.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR008985; ConA-like lec_gl.
DR Pfam; PF00262; calreticulin_1.
DR PIRSF; PIRSF002356; Calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
KW SIGNAL
FT CHAIN 1 19 POTENTIAL.
FT DOMAIN 20 424 CALRETICULIN.
FT REPEAT 191 257 4 X 12 AA APPROXIMATE REPEATS.
FT REPEAT 211 222 1-1.
FT REPEAT 227 238 1-2.
FT REPEAT 246 257 1-3.
FT REPEAT 260 298 3 X 11 AA APPROXIMATE REPEATS.
FT REPEAT 260 298 2-1.
FT REPEAT 270 284 2-2.
FT REPEAT 288 298 2-3.
FT DISULFID 105 137 BY SIMILARITY.
FT SITE 421 424 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 424 AA; 48350 MW; BAF273694FB6FC37 CRC64;

Query Match 57.6%; Score 148.5; DB 1; Length 424;
Best Local Similarity 53.1%; Fred. No. 1.2e-11;
Matches 26; Conservative 12; Mismatches 10; Indels 1; Gaps 1;

OY 1 NYKGNVLINKDI-RCKDDETHLYTLVRPDNTYEVKIDNSQVSGSL 48
Db 148 NYKGNVHLIKKINKVETDQLTHQYTLVSPDNTYVLDVNDKIQAGNL 196

RESULT 14
CRTC_MOUSE
ID CRTC3_MOUSE STANDARD; PRT; 380 AA.
AC Q9D9Q6;

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DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Calreticulin 3 precursor (Calreticulin 2).
GN CALR3 OR CRT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [2]
RC IDENTIFICATION, AND TISSUE SPECIFICITY.
RA MEDLINE=22271577; PubMed=12384296;
RA Persson S., Rosenquist M., Sommarin M.;
RT "Identification of a novel calreticulin isoform (Crt2) in human and
RT mouse.";
RL Gene 297:151-158 (2002).
CC -1- FUNCTION: Ca(2+)-binding chaperone (By similarity).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
CC -1- SIMILARITY: Belongs to the calreticulin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DE EMBL: AK006582; BAB24660.1;
DR MGD; MGI:1920566; Calr3.
DR InterPro; IPR009033; Calret_calmex_P.
DR InterPro; IPR001580; Calreticulin_2.
DR InterPro; IPR008985; ConA-like lec_gl.
DR InterPro; IPR000886; ER_target_S.
DR Pfam; PF00262; calreticulin; 1.
DR PIRSF; PIRSF002356; Calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00804; CALRETICULIN_1; 1.
DR PROSITE; PS00805; CALRETICULIN_2; 1.
DR PROSITE; PS00014; ER_TARGET; FALSE NEG.
DR Chaperone; Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
KW SIGNAL
FT CHAIN 1 19 POTENTIAL.
FT DOMAIN 20 380 CALRETICULIN 3.
FT REPEAT 198 291 N-DOMAIN.
FT REPEAT 292 380 P-DOMAIN.
FT REPEAT 191 292 C-DOMAIN.
FT REPEAT 191 292 4 X APPROXIMATE REPEATS.
FT REPEAT 191 292 1-1.

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FT REPEAT 209 220 1-2.
FT REPEAT 221 231 1-3.
FT REPEAT 235 246 1-4.
FT DOMAIN 250 280 3 X APPROXIMATE REPEATS.
FT REPEAT 250 256 2-1.
FT REPEAT 260 268 2-2.
FT REPEAT 270 288 2-3.
FT SITE 377 380 PREVENT SECRETION FROM ER (POTENTIAL).
FT DISULFID 137 163 BY SIMILARITY.
FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 380 AA; 44197 MW; B13BC4ADB1B0442 CRC64;

Query Match 57.0%; Score 147; DB 1; Length 380;
Best Local Similarity 69.2%; Pred. No. 1.7e-11; Indels 0; Gaps 0;
Matches 27; Conservative 5; Mismatches 7;

QY 11 KDRCRCKDDETHLYTVRPDNTYEVKIDNSQVSGSLE 49
Db 159 KPICRCKVDGTHLYTLIRPDLSEYEVKVDQSQSIESGSI 197

RESULT 15
CRT3 HUMAN
ID CRT3 HUMAN STANDARD; PRT; 384 AA.
AC Q96L12; Q96L13;
DT 28-FEB-2003 (Rel. 41, Created)
DE 28-FEB-2003 (Rel. 41, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Calreticulin 3 precursor (calreticulin 2).
GN CALR3 OR CRT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
RA Houta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
RA Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA Sugiyama T., Irie K., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA Kawakami B., Nagai K., Isogai T., Sugano S.;
RA "NEDO human cDNA sequencing project";
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grumwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP IDENTIFICATION, AND TISSUE SPECIFICITY.
RN MEDLINE=22271577; PubMed=12384296;
RX

```

```

RA Persson S., Rosenquist M., Sommarin M.;
RT "Identification of a novel calreticulin isoform (Crt2) in human and
mouse.";
RL Gene 297:151-158 (2002).
CC -!- FUNCTION: Ca(2+)-binding chaperone (By similarity). (By similarity).
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
CC -!- TISSUE SPECIFICITY: Testis specific.
CC -!- SIMILARITY: Belongs to the calreticulin family.
CC
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CC
CC EMBL; AK058084; BAB71655.1; -
CC EMBL; BC014595; AAL14595.1; -
CC GenBank; HGNC:20407; CALR3.
CC InterPro; IPR009033; Calret calnex P.
CC InterPro; IPR001580; Calreticulin_
CC InterPro; IPR008985; ConA-like lec_gl.
CC InterPro; IPR008866; ER_target_S.
CC Pfam; PF00262; calreticulin; 1.
CC PRINTS; PIRSF002356; Calreticulin.
CC PRINTS; PRC0626; CALRETICULIN.
CC PRODom; PRC01866; Calreticulin; 1.
CC PROSITE; PS00803; CALRETICULIN_1; 1.
CC PROSITE; PS00804; CALRETICULIN_2; 1.
CC PROSITE; PS00014; ER_TARGET; 1.
CC KW Chaperone; Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 384 CALRETICULIN 3.
FT DOMAIN 20 197 N-DOMAIN.
FT DOMAIN 198 294 P-DOMAIN.
FT DOMAIN 235 384 C-DOMAIN.
FT DOMAIN 191 245 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 208 219 1-2.
FT REPEAT 221 230 1-3.
FT REPEAT 234 245 1-4.
FT DOMAIN 249 283 3 X APPROXIMATE REPEATS.
FT REPEAT 249 259 2-1.
FT REPEAT 253 271 2-2.
FT REPEAT 273 362 2-3.
FT DOMAIN 357 384 POLY-GLU.
FT SITE 381 384 PREVENT SECRETION FROM ER (POTENTIAL).
FT DISULFID 137 163 BY SIMILARITY.
FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 8 8 F > L (IN REF. 1).
SQ SEQUENCE 384 AA; 45029 MW; 33F7CB523FEFF187 CRC64;

Query Match 56.2%; Score 145; DB 1; Length 384;
Best Local Similarity 59.2%; Pred. No. 3e-11;
Matches 29; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 1 NYGKQVNLINKDRCRCKDDETHLYTVRPDNTYEVKIDNSQVSGSLE 49
Db 149 HFZKZYHKNKLRCKVDGTHLYTLIRPDLSEYEVKVDQSQSIESGSI 197

Search completed: October 4, 2004, 13:04:01
Job time : 7.20588 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2004, 12:52:42 ; Search time 29.6882 Seconds
(without alignments)
520.758 Million cell updates/sec

Title: US-09-807-148-6
Perfect score: 258
Sequence: 1 NYGKNVLINKDIRCKDDEF.....PDNTYEVKIDNSQVESGSLE 49

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Result No.	Score	Query Match	Length	ID	Description
1	234	90.7	318	13 Q9PTX7	Q9ptx7 lampetra re
2	226	87.6	343	13 Q91711	Q91711 xenopus lae
3	226	87.6	411	13 Q91710	Q91710 xenopus lae
4	226	87.6	413	13 Q7ZWU8	Q7zwu8 xenopus lae
5	226	87.6	418	13 Q7ZXV3	Q7zxv3 xenopus lae
6	221	85.7	405	5 Q26268	Q26268 aplysia cal
7	217	84.1	403	5 Q81S63	Q81s63 cotesia rub
8	215	83.3	407	5 Q86G72	Q86g72 dermacentor
9	215	83.3	417	13 Q9PUC1	Q9puc1 brachydanio
10	212	82.2	423	13 Q7SZM3	Q7szm3 ictalurus p
11	211	81.8	406	5 Q8WR36	Q8wr36 anopheles g
12	210	81.4	417	13 Q802X3	Q802x3 brachydanio
13	210	81.4	419	13 Q88984	Q88984 rana rugosa
14	210	81.4	421	5 Q9U6S0	Q9u6s0 strongyloce
15	209	81.0	406	5 Q9U916	Q9u916 drosophila
16	209	81.0	411	5 Q8MWP3	Q8mwp3 boophilus m

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
17	208	80.6	398	5 Q869E0	Q869e0 bombyx mori
18	208	80.6	398	5 Q7ZIE6	Q7zie6 bombyx mori
19	207	80.2	397	5 Q8WPG8	Q8wpg8 galliera me
20	207	80.2	410	5 Q16893	Q16893 amblyomma a
21	205	79.5	407	5 Q8T9U3	Q8t9u3 aedes aegyp
22	204	79.1	403	5 Q76961	Q76961 necator ame
23	196	76.0	350	5 Q26514	Q26514 schistosoma
24	196	76.0	396	5 Q45034	Q45034 schistosoma
25	194	75.2	415	5 Q8WRU9	Q8wru9 meloidosyne
26	189	73.3	387	5 Q97372	Q97372 dirofilaria
27	183	70.9	375	5 Q18478	Q18478 litomosolde
28	180	69.8	395	5 Q96722	Q96722 taenia soli
29	179	69.4	321	13 Q9U5G0	Q9u5g0 eptatretus
30	148	57.4	421	10 Q43712	Q43712 zea mays (m
31	147	57.0	137	11 Q9D373	Q9d373 mus musculu
32	147	57.0	272	11 Q8BL82	Q8bl82 mus musculu
33	147	57.0	442	10 Q7Y140	Q7y140 oryza sativ
34	146	56.6	321	10 Q41799	Q41799 zea mays (m
35	144	55.8	412	10 Q40040	Q40040 hordeum vul
36	144	55.8	415	10 Q40041	Q40041 hordeum vul
37	142	55.0	425	10 Q8LJ85	Q8lj85 oryza sativ
38	140.5	54.5	427	10 Q9FVY2	Q9fyv2 pinus taeda
39	139	53.9	214	4 Q9UDG2	Q9udg2 homo sapien
40	138	53.5	416	10 Q8H792	Q8h792 arabidopsis
41	136	52.7	263	10 Q84M42	Q84m42 oryza sativ
42	135	52.3	240	10 Q9ST29	Q9st29 solanum mel
43	135	52.3	389	10 Q40567	Q40567 nicotiana t
44	135	52.3	424	10 Q94RW7	Q94aw7 arabidopsis
45	135	52.3	424	10 Q8LC80	Q8lc80 arabidopsis

ALIGNMENTS

RESULT 1

Q9PTX7 PRELIMINARY; PRT; 318 AA.

ID Q9PTX7

AC Q9PTX7; 01-MAY-2000 (TREMELrel. 13, Created)

DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE Calreticulin (fragment).

OS Lampetra reissneri (far Eastern brook lamprey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;

OC Petromyzontiformes; Petromyzontidae; Lethenteron.

OX NCBI_TaxID=7753;

RN [1] Mol. Evol. 49:729-735(1999).

RP SEQUENCE FROM N.A.

RX MEDLINE=2063780; PubMed=10594174; Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.; "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded genes.";

RT J. Mol. Evol. 49:729-735(1999).

RL ENBL; AB025328; BAA88481.1; GO; GO:0005514; F:calcium ion storage activity; IEA.

DR InterPro; IPR001580; Calreticulin.

DR InterPro; IPR009033; Calret. calnex.P.

DR InterPro; IPR008985; ConA like lec_gl.

DR InterPro; IPR000886; ER target_S.

DR Pfam; PF00362; calreticulin_1.

DR PRINIS; PR00626; CALRETICULIN.

DR ProDom; PD001866; Calreticulin; 1.

DR PROSITE; PS00804; CALRETICULIN-2; 1.

DR PROSITE; PS00805; CALRETICULIN REPEAT; 3.

DR PROSITE; PS00014; ER TARGET; 1.

DR NON_TER 1.

FT NON_TER 1.

SQ SEQUENCE 318 AA; 36997 MW; C88102EA1CAC1506 CRC64;

Query Match 90.7%; Score 234; DB 13; Length 318;
Best local similarity 89.8%; Pred. No. 2.7e-21;
Matches 44; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NYGKNVLINKDIRCKDDEFHTLYTLVPRDNTYEVKIDNSQVESGSLE 49

QY	1	NYKGNVLINKDIRCKDDFTHLYTLIVRPDNTYEVKIDNSQVSGSLE	49
Db	145	NYKGNLLVKKDIRCKDDVFSHLYTLIVRPDNTYEVKIDNEKXESGDLE	193
RESULT 7			
ID	Q81S63	PRELIMINARY;	PRT; 403 AA.
AC	Q81S63;		
DT	01-MAR-2003	(T-EMBLrel. 23, Created)	
DT	01-MAR-2003	(T-EMBLrel. 23, Last sequence update)	
DT	01-OCT-2003	(T-EMBLrel. 25, Last annotation update)	
DE	DE	Calreticulin.	
OS	Cotesia rubecula.		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae		
OC	Braconidae; Microgastriinae; Cotesia.		
OC	NCBI_Taxid=32392;		
OC	[1]		
RP	SEQUENCE FROM N.A.		
RA	Asgari S., Zhang G., Schmidt O.;		
RT	"Polynavirus particle proteins with similarities to molecular		
RT	chaperons, heat shock protein 70 and calreticulin.";		
RL	Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY150370; AN73309.1;		
DR	GO; GO:0005514; F:calcium ion storage activity; IEA.		
DR	InterPro; IPR001580; Calreticulin.		
DR	InterPro; IPR009033; Calret calnex P.		
DR	InterPro; IPR008985; ConA like lec_gl.		
DR	InterPro; IPR000886; ER target_S.		
DR	Pfam; PF00262; calreticulin; 1.		
DR	PRINTS; PR00626; CALRETICULIN.		
DR	PRODOM; PD001866; Calreticulin; 1.		
DR	PROSITE; PS00803; CALRETICULIN 1; 1.		
DR	PROSITE; PS00804; CALRETICULIN 2; 1.		
DR	PROSITE; PS00805; CALRETICULIN REPEAT; 2.		
DR	PROSITE; PS00014; ER TARGET; 1.		
DR	SEQUENCE 403 AA; 46550 MW; 259D771A822DB126 CRC64;		
QY	1	NYKGNVLINKDIRCKDDFTHLYTLIVRPDNTYEVKIDNSQVSGSLE	49
Db	148	NYKGNLLVKKDIRCKDDVFTHLYTLIVRPDNTYEVLDNEKVESGELE	196
Query Match 84.1%; Score 217; DB 5; Length 403;			
Best Local Similarity 81.6%; Pred. No. 4.9e-19;			
Matches 40; Conservative 4; Mismatches 5; Indels 0;			
RESULT 8			
ID	Q86G72	PRELIMINARY;	PRT; 407 AA.
AC	Q86G72;		
DT	01-JUN-2003	(T-EMBLrel. 24, Created)	
DT	01-JUN-2003	(T-EMBLrel. 24, Last sequence update)	
DT	01-OCT-2003	(T-EMBLrel. 25, Last annotation update)	
DE	DE	Calreticulin.	
OS	Dermacentor variabilis.		
OC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;		
OC	Parasitiformes; Ixodida; Ixodidae; Dermacentor.		
OC	NCBI_Taxid=34621;		
OC	[1]		
RP	SEQUENCE FROM N.A.		
RA	Simsen J.A., Mulenga A., Macaluso K.R., Azad A.F.;		
RT	"Molecular characterization of Dermacentor variabilis calretic		
RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY241957; AAC092278.1;		
DR	GO; GO:0005514; F:calcium ion storage activity; IEA.		
DR	InterPro; IPR001580; Calreticulin.		
DR	InterPro; IPR009033; Calret calnex P.		
DR	InterPro; IPR008985; ConA like lec_gl.		
DR	InterPro; IPR000886; ER target_S.		
DR	Pfam; PF00262; calreticulin; 1.		

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DR PRINTS; PRO0626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; 1.
SQ SEQUENCE 407 AA; 47190 MW; FFE8063AC49446E8 CRC64;

Query Match      83.3%; Score 215; DB 5; Length 407;
Best Local Similarity 81.6%; Pred. No. 8.9e-19;
Matches 40; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 NYKGNVLINKDKDDFTHLYTLVPRDNTYEVKIDNSQVSGSLE 49
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 148 NYKGQNLINKDKDDVFTHLYTLVPRDNTYQVKIDNEVKGGELE 196

RESULT 9
Q9PUC1 ID Q9PUC1 PRELIMINARY; PRT; 417 AA.
AC Q9PUC1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calreticulin.
GN CALR
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20190113; PubMed=10660676;
RA Rubinstein A.L.; Lee D.; Luo R.; Henion P.D.; Halpern M.E.;
RT "Genes dependent on zebrafish cyclops function identified by AFLP
RT differential gene expression screen.";
RL Genesis 26:86-97(2000).
DR EMBL; AF195882; RA13700.1; -.
DR ZFIN; ZDB-GENE-000208-17; Calr.
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret. calnex P.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR000886; ER target_S.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; 1.
SQ SEQUENCE 417 AA; 48723 MW; 2000C5B4004699B6 CRC64;

Query Match      83.3%; Score 215; DB 13; Length 417;
Best Local Similarity 81.6%; Pred. No. 9.1e-19;
Matches 40; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 NYKGNVLINKDKDDFTHLYTLVPRDNTYEVKIDNSQVSGSLE 49
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 149 NYKGQNLINKDKDDVFTHLYTLVPRDNTYQVKIDNEVKGGELE 197

RESULT 10
Q7SZM3 ID Q7SZM3 PRELIMINARY; PRT; 423 AA.
AC Q7SZM3
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ER-resident chaperone calreticulin.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RA McConnell T.J.; Pitzer J.E.;
RT "Calreticulin in the Channel Catfish, Ictalurus punctatus.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY342298; AAQ19852.1; -.
SQ SEQUENCE 423 AA; 49186 MW; ED7CBA5C1FBC07EB CRC64;

Query Match      82.2%; Score 212; DB 13; Length 423;
Best Local Similarity 81.6%; Pred. No. 2.2e-19;
Matches 40; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 NYKGNVLINKDKDDFTHLYTLVPRDNTYEVKIDNSQVSGSLE 49
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 149 NYKGQNLINKDKDDFTHLYTLVPRDNTYQVKIDNEVKGGELE 197

RESULT 11
Q8WR36 ID Q8WR36 PRELIMINARY; PRT; 406 AA.
AC Q8WR36
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calreticulin.
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=7165;
RN [1]
RP SEQUENCE FROM N.A.
RA Francisetti I.M.; Valenzuela J.G.; Ribeiro J.M.;
RT "Towards a catalog for genes and proteins from the salivary gland of
RT the malaria vector, Anopheles gambiae.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF457551; AAL68781.1; -.
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret. calnex P.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR000886; ER target_S.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; 1.
SQ SEQUENCE 406 AA; 46285 MW; 85068FBBCA9931F1 CRC64;

Query Match      81.8%; Score 211; DB 5; Length 406;
Best Local Similarity 81.6%; Pred. No. 2.8e-18;
Matches 40; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 NYKGNVLINKDKDDFTHLYTLVPRDNTYEVKIDNSQVSGSLE 49
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 146 SYKGQNLINKDKDDVFTHLYTLVPRDNTYQVKIDNEVKGGELE 194

RESULT 12
Q802X3 ID Q802X3 PRELIMINARY; PRT; 417 AA.
AC Q802X3
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to calreticulin.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;

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Best Local Similarity 81.6%; Pred. No. 3.9e-18; Gaps 0;
Matches 40; Conservative 5; Mismatches 4; Indels 0;

QY 1 NYKGNVLINKDCKDDETHLYTLVPRDNTYEVKIDNSQVSGSLE 49
DB 150 NYKGNVLINKDCKDDETHLYTLVPRDNTYEVKIDNSQVSGSLE 198

RESULT 14
Q9U916 PRELIMINARY; PRT; 421 AA.
AC Q9U916
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calreticulin precursor.
GN CALRET.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC Strongylocentrotus.
OC NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RA Susan J.M., Just M.L., Lennarz W.J.;
RT "Cloning and Characterization of Alphas Integrin and Calreticulin in
RT Embryos of the Sea Urchin."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF177915; AAD55725.1;
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret calnex P.
DR InterPro; IPR008985; ConA-like lec_gl.
DR InterPro; IPR008866; ER_target_S.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PROSITE; PS001866; Calreticulin; 1.
DR PROSITE; PS00804; CALRETICULIN 2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; 1.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 421 CALRETICULIN.
SQ SEQUENCE 421 AA; 48822 MW; 172C664F59F41F93 CRC64;

Query Match 81.4%; Score 210; DB 5; Length 421;
Best Local Similarity 75.5%; Pred. No. 3.9e-18; Gaps 0;
Matches 37; Conservative 8; Mismatches 4; Indels 0;

QY 1 NYKGNVLINKDCKDDETHLYTLVPRDNTYEVKIDNSQVSGSLE 49
DB 148 NYKGNVLINKDCKDDETHLYTLVPRDNTYEVKIDNSQVSGSLE 196

RESULT 15
Q9U916 PRELIMINARY; PRT; 406 AA.
ID Q9U916
AC Q9U916
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calreticulin.
GN CRC OR CG9429.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=OREGON-R;
RC Dodo K., Sakoyama Y., Gamo S.;
RA "Drosophila melanogaster calreticulin for mRNA."
RT

Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046906; AAH46906.1;
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret calnex P.
DR InterPro; IPR008985; ConA-like lec_gl.
DR InterPro; IPR008866; ER_target_S.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN 1; 1.
DR PROSITE; PS00804; CALRETICULIN 2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; 1.
SQ SEQUENCE 417 AA; 48259 MW; F7D11614F4319586 CRC64;

Query Match 81.4%; Score 210; DB 13; Length 417;
Best Local Similarity 79.6%; Pred. No. 3.9e-18; Gaps 0;
Matches 39; Conservative 4; Mismatches 6; Indels 0;

QY 1 NYKGNVLINKDCKDDETHLYTLVPRDNTYEVKIDNSQVSGSLE 49
DB 150 NYKGNVLINKDCKDDETHLYTLVPRDNTYEVKIDNSQVSGSLE 198

RESULT 13
Q98984 PRELIMINARY; PRT; 419 AA.
ID Q98984
AC Q98984
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calreticulin.
OS Rana rugosa (Wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OC NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96234004; PubMed=8654561;
RA Yamamoto S., Nakamura M.;
RT "Calnexin: its molecular cloning and expression in the liver of the
RT frog, Rana rugosa."
RL FEBS Lett. 387:27-32(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96387817; PubMed=8795287;
RA Yamamoto S., Kondo Y., Hanada H., Nakamura M.;
RT "Strong expression of the calreticulin gene in the liver of Rana
RT rugosa tadpoles, but not adult frogs."
RL J. Exp. Zool. 275:431-443(1996).
DR EMBL; D78589; BAAL1425.1;
DR PIR; S71343; S71343.
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret calnex P.
DR InterPro; IPR008985; ConA-like lec_gl.
DR InterPro; IPR008866; ER_target_S.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN 1; 1.
DR PROSITE; PS00804; CALRETICULIN 2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; 1.
SQ SEQUENCE 419 AA; 48658 MW; 2C857036769673BF CRC64;

Query Match 81.4%; Score 210; DB 13; Length 419;

Submitted (JAN-1997) to the ENBL/GenBank/DBJ databases.

EMBL; AB000718; EAA85379.1; -.
FlyBase; Fgnm005585; Crc.
GC; GO:0007417; P:central nervous system development; IMP
InterPro; IPR001580; Calreticulin.
InterPro; IPR009033; Calret calnex P.
InterPro; IPR008985; ConA like lec_gi.
InterPro; IPR008886; ER target_S_gi.
Pfam; PF00262; calreticulin; 1.
PRINTS; PR00626; CALRETICULIN.
ProDom; PD001866; Calreticulin; 1.
PROSITE; PS00803; CALRETICULIN 1; 1.
PROSITE; PS00804; CALRETICULIN 2; 1.
PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
PROSITE; PS00014; ER_TARGET; 1.
SEQUENCE 406 AA; 46809 MW; 68BA49A6B81CC427 CRC64;

Query Match	81.0%;	Score 209;	DB 5;	Length 406;
Best Local Similarity	79.6%;	Pred. No. 5.1e-18;		
Matches	39;	Conservative	5; Mismatches	5; Indels 0; Gaps 0;

	QY	Db
1	NYGKNVLINKDIRCKODEFTHLYTLIVRPDNTYEVKIDNSQVESGSL	49
149	SYGKNHLISKDIRCKDDVYTHFYTLIVRPDNTYEVLIIDNEKVESGNLE	197

Search completed: October 4, 2004, 13:05:52
Job time : 29.6882 secs

01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to calreticulin.
Xenopus laevis (African clawed frog).
Amphibia; Batrachia; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=8355;
[1]
SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046699; AAH46699.1; -
GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret calnex P.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR000886; ER target S.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER TARGET; 1.
SQ SEQUENCE 413 AA; 48521 MW; DE002F8F0523772B CRC64;

Query Match 87.4%; Score 278; DB 13; Length 413;
Best Local Similarity 88.3%; Pred. No. 1.3e-24;
Matches 53; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 GPGTKKHVIFNYKGNVLINCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 60
Db 139 GPPTKXHVIFQYKKNLQINCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 198

RESULT 6
Q7ZXY3
ID Q7ZXY3 PRELIMINARY; PRT; 418 AA.
AC Q7ZXY3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to calreticulin.
OS Xenopus laevis (African clawed frog).
OC Amphibia; Batrachia; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=8355;
[1]
SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044068; AAH44068.1; -
GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret calnex P.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR000886; ER target S.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER TARGET; 1.
SQ SEQUENCE 418 AA; 49028 MW; 731C1C9AA0BF9A53 CRC64;

Query Match 87.4%; Score 278; DB 13; Length 418;
Best Local Similarity 88.3%; Pred. No. 1.3e-24;
Matches 53; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 GPGTKKHVIFNYKGNVLINCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 60
Db 139 GPPTKXHVIFQYKKNLQINCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 198

RESULT 7
Q8IS63
ID Q8IS63 PRELIMINARY; PRT; 403 AA.
AC Q8IS63;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calreticulin.
OS Cotesia rubecula.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;
OC Braconidae; Microgasterinae; Cotesia.
OC NCB_TaxID=32392;
RN [1]
SEQUENCE FROM N.A.
RA Asgari S., Zhang G., Schmidt C.;
RT "polydnavirus particle proteins with similarities to molecular
chaperons, heat shock protein 70 and calreticulin."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF150370; AAN73309.1; -
GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret calnex P.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR000886; ER target S.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER TARGET; 1.
SQ SEQUENCE 403 AA; 46550 MW; 259D771A822DB126 CRC64;

Query Match 86.8%; Score 276; DB 5; Length 403;
Best Local Similarity 83.3%; Pred. No. 2.2e-24;
Matches 50; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 GPGTKKHVIFNYKGNVLINCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 60
Db 137 GPPTKXHVIFNYKGNVLINCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 196

RESULT 8
Q86G72
ID Q86G72 PRELIMINARY; PRT; 407 AA.
AC Q86G72;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calreticulin.
OS Dermacentor variabilis.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Dermacentor.
OC NCB_TaxID=34621;
RN [1]
SEQUENCE FROM N.A.
RA Simser J.A., Muelenga A., Macaluso K.R., Azad A.F.;
RT "Molecular characterization of Dermacentor variabilis calreticulin."
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AZ241957; AAC92478.1; -
GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret calnex P.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR000886; ER target S.
DR Pfam; PF00262; calreticulin; 1.
SQ SEQUENCE 407 AA; 46550 MW; 259D771A822DB126 CRC64;

DR PRINTS; PR00626; CALRETICULIN
 DR PRODOM; PD001866; Calreticulin; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 DR PROSITE; PS00014; ER_TARGET; 1.
 SQ SEQUENCE 407 AA; 47190 MW; FFE8063AC4946E8 CRC64;
 Query Match 86.58; Score 275; DB 5; Length 407;
 Best Local Similarity 85.0%; Pred. No. 2.9e-24;
 Matches 51; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 QY 1 GPGTKKVVHVFNYKGNVLINKDIRCKDDFFTHLYTLVVRPNTYEVKIDNSQVSGSLE 60
 DB 137 GPGTKKVVHVFNYKGNVLINKDIRCKDDFFTHLYTLVVRPNTYEVKIDNSQVSGSLE 196
 RESULT 9
 Q8WR36 PRELIMINARY; PRT; 406 AA.
 AC Q8WR36
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Calreticulin.
 OS Anopheles gambiae (African malaria mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hexapoda; Insecta; Culicoidea; Anopheles.
 OX NCBI_TaxID=7165;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Francischetti I.M., Valenzuela J.G., Ribeiro J.M.;
 RT "Towards a catalog for genes and proteins from the salivary gland of
 RL the malaria vector, Anopheles gambiae.";
 DR EMBL; AF457551; AAL68781.1; - - - - -
 DR GO; GO:0005514; F:calcium ion storage activity; IEA.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR009033; Calret_calmex_P.
 DR InterPro; IPR008985; ConA like lec_gl.
 DR InterPro; IPR000886; ER target_S.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR PRODOM; PD001866; Calreticulin; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 DR PROSITE; PS00014; ER_TARGET; 1.
 SQ SEQUENCE 406 AA; 46285 MW; 85068FBBCA9931F1 CRC64;
 Query Match 85.2%; Score 271; DB 5; Length 406;
 Best Local Similarity 85.0%; Pred. No. 8.7e-24;
 Matches 51; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 QY 1 GPGTKKVVHVFNYKGNVLINKDIRCKDDFFTHLYTLVVRPNTYEVKIDNSQVSGSLE 60
 DB 135 GPGTKKVVHVFNYKGNVLINKDIRCKDDFFTHLYTLVVRADNTYEVLDNEKVESSGLE 194
 RESULT 10
 Q9U6S0 PRELIMINARY; PRT; 421 AA.
 AC Q9U6S0
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Calreticulin precursor.
 GN CALRET.
 OS Strongylocentrotus purpuratus (Purple sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Echinoidea; Echinacea; Echinoida; Strongylocentrotidae;
 OC Strongylocentrotus.
 OX NCBI_TaxID=7668;
 RP SEQUENCE FROM N.A.
 RA Dodo K., Sakoyama Y., Gamo S.;
 RT "Drosophila melanogaster calreticulin for mRNA.";
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB000718; BAA85379.1; - - - - -
 DR FlyBase; FBgn0005585; CrC.
 DR GO; GO:0007417; P:central nervous system development; IMP.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR009033; Calret_calmex_P.
 DR InterPro; IPR008985; ConA like lec_gl.
 DR InterPro; IPR000886; ER target_S.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR PRODOM; PD001866; Calreticulin; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 DR PROSITE; PS00014; ER_TARGET; 1.
 SQ SEQUENCE 406 AA; 46809 MW; 68BA49A6B81CC427 CRC64;
 Query Match 84.6%; Score 269; DB 5; Length 406;
 Best Local Similarity 83.3%; Pred. No. 1.5e-23;
 Matches 50; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 1 GPGTKKVVHVFNYKGNVLINKDIRCKDDFFTHLYTLVVRPNTYEVKIDNSQVSGSLE 60

RN SEQUENCE FROM N.A.
 RP Susan J.M., Just M.L., Lennarz W.J.;
 RT "Cloning and Characterization of Alpha Integrin and Calreticulin in
 RT Embryos of the Sea Urchin.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF177915; AAD55725.1; - - - - -
 DR GO; GO:0005514; F:calcium ion storage activity; IEA.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR009033; Calret_calmex_P.
 DR InterPro; IPR008985; ConA like lec_gl.
 DR InterPro; IPR000886; ER target_S.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR PRODOM; PD001866; Calreticulin; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 DR PROSITE; PS00014; ER_TARGET; 1.
 KW Signal.
 FT SIGNAL.
 FT CHAIN.
 FT SIGNAL.
 FT CHAIN.
 SQ SEQUENCE 421 AA; 48822 MW; 172C664F59F41F93 CRC64;
 Query Match 84.9%; Score 270; DB 5; Length 421;
 Best Local Similarity 80.0%; Pred. No. 1.2e-23;
 Matches 48; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
 QY 1 GPGTKKVVHVFNYKGNVLINKDIRCKDDFFTHLYTLVVRPNTYEVKIDNSQVSGSLE 60
 DB 137 GPGTKKVVHVFNYKGNVLINKDIRCKDDFFTHLYTLVVRPNTYEVKIDNSQVSGSLE 196
 RESULT 11
 Q9U916 PRELIMINARY; PRT; 406 AA.
 AC Q9U916
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Calreticulin.
 GN CRC OR CG9429.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dodo K., Sakoyama Y., Gamo S.;
 RT "Drosophila melanogaster calreticulin for mRNA.";
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB000718; BAA85379.1; - - - - -
 DR FlyBase; FBgn0005585; CrC.
 DR GO; GO:0007417; P:central nervous system development; IMP.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR009033; Calret_calmex_P.
 DR InterPro; IPR008985; ConA like lec_gl.
 DR InterPro; IPR000886; ER target_S.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR PRODOM; PD001866; Calreticulin; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 DR PROSITE; PS00014; ER_TARGET; 1.
 SQ SEQUENCE 406 AA; 46809 MW; 68BA49A6B81CC427 CRC64;
 Query Match 84.6%; Score 269; DB 5; Length 406;
 Best Local Similarity 83.3%; Pred. No. 1.5e-23;
 Matches 50; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 1 GPGTKKVVHVFNYKGNVLINKDIRCKDDFFTHLYTLVVRPNTYEVKIDNSQVSGSLE 60

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138 GPGTKKVHVFYSYKGNHLISKDIRCKDDVYTHFTLVIRPDNTYEVLIDNKEVESGDNLE 197

RESULT 12
Q869E0 PRELIMINARY; PRT; 398 AA.
Q869E0;
AC Q869E0;
01-JUN-2003 (TREMBLrel. 24, Created)
01-JUN-2003 (TRMBLrel. 24, Last sequence update)
01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Calreticulin.
CRL.
Bombyx mori (Silk moth).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
Bombycidae; Bombyx.
NCBI_TaxID=7091;
[1]
RP SEQUENCE FROM N.A.
STRAIN=DAIZO; TISSUE=Fat body;
Takashi T., Yamashita I.;
"Calreticulum expressed in fatbody of Bombyx mori.";
Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AB090887; BACS7964.1; -.
GO: GO:0005514; F:calcium ion storage activity; IEA.
InterPro; IPR001580; Calreticulin.
InterPro; IPR009033; Calret_calmex_P.
InterPro; IPR009885; Cnsl_likelec_g1.
InterPro; IPR000886; ER_target_S.
Pfam; PF00262; calreticulin; 1.
PRINTS; P00626; CALRETICULIN.
ProDom; PD001866; Calreticulin; 1.
PROSITE; PS00803; CALRETICULIN_1; 1.
PROSITE; PS00804; CALRETICULIN_2; 1.
PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
PROSITE; PS00014; ER_TARGET; 1.
SEQUENCE 398 AA; 45768 MW; 522480CF9BD83306 CRC64;

Query Match      84.3%; Score 268; DB 5; Length 398;
Best Local Similarity    83.3%; Pred.No.1.9e-23;
Matches 50; Conservative 4; Mismatches 6; Indels 0; Gaps 0

Oy   1 GPGTKKHVVFNFKGVNLINKDKRCDDFTHLYTLIVRPDNTYEKLIDNSOVESGSLE 60
Db   138 GPGTKKHVVFIYSYKGNHLIKDIRCKDDVYTHLYTLIVFPDNTYEVLIDNKEVESGDLE 197
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RESULT 13
Q7Z1E6
ID Q7Z1E6 PRELIMINARY; PRT; 398 AA.
AC Q7Z1E6;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Calreticulin.
OS Bombyx mori (Silk moth);
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Bombycoidea;
OC Bombycidae; Bombyx.
OC NCBI_TaxID=7091;
RN
RP SEQUENCE FROM N.A.
RA Kim S.R., Lee K.S., Kim I., Kang S.W., Nho S.K., Sohn H.D., Jin B.R.;
RT "Molecular cloning of a cDNA encoding putative calreticulin from the
RT silkworm, Bombyx mori.";
RL Int. J. Indust. Entomol. 6:93-97(2003).
DR EMBL; AV297158; AAP50845.1; -.
SQ SEQUENCE 398 AA; 45801 MW; 0BC049839F5950EA CRC64;

Query Match 84.3%; Score 268; DB 5; Length 398;
Best Local Similarity 83.3%; Pred. No. 1,9e-23;
Accession Match 54; Accession No. Gaus

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RP SEQUENCE FROM N.A.
 RC TISSUE=Salivary gland;
 RA Jaworski D.C.;
 RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Salivary gland;
 RA Fain-Thornton J.M., Jaworski D.C., Needham G.R.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U07708; AAC79094.1; -;
 DR GO: GO:0005514; F:calcium ion storage activity; IEA.
 DR InterPro: IPR001580; Calreticulin.
 DR InterPro: IPR009033; Calret_calmex_P.
 DR InterPro: IPR008985; ConA_like Lec_gl.
 DR InterPro: IPR000886; ER_target_S.
 DR Pfam: PF00262; calreticulin; 1.
 DR PRINTS: PR00626; CALRETICULIN.
 DR ProDom: PD001866; Calreticulin; 1.
 DR PROSITE: PS00803; CALRETICULIN_1; 1.
 DR PROSITE: PS00805; CALRETICULIN_REPEAT; 3.
 DR PROSITE: PS00014; ER_TARGET; 1.
 SQ SEQUENCE 410 AA; 47485 MW; 32CCB8750A17DC54 CRC64;

Query Match 84.0%; Score 267; DB 5; Length 410;
 Best Local Similarity 83.3%; Pred. No. 2.6e-23;
 Matches 50; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 Qy 1 GPCTKKVHVFNYKGNVLNKDIRCKDBEFTHLYTLIVRPDNTVEVKIDNSQVESGSLE 60
 Db 137 GPCTKKVHVFNYKGNHNLNKDIRCKDDVFTHLYTLIVKPDNTYVWKIDNEVAKGELE 196

Search completed: October 4, 2004, 13:05:52
 Job time : 36.3529 secs

OM protein - protein search, using sw model

Run on: October 4, 2004, 12:50:22 ; Search time 45.5294 Seconds
(without alignments)
372.349 Million cell updates/sec

Title: US-09-807-148-8

Perfect score: 318

Sequence: 1 GFGTKKHVIFNYKGNVLI.....PDNTYEVKIDNSQVESGSL 60

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_28Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	318	100.0	60	3	AAY92354 Recombina
2	318	100.0	61	3	AAY92352 Recombina
3	318	100.0	180	3	AAY92351 Human vas
4	318	100.0	280	3	AAY92355 Recombina
5	318	100.0	400	3	AAY92350 Recombina
6	318	100.0	401	2	AAW11156 Calreticu
7	318	100.0	416	7	Ades6306 Rat Prote
8	318	100.0	416	7	Ades6310 Rat Prote
9	318	100.0	417	1	AP92276 60 kD Ro
10	318	100.0	417	2	AAY00927 Calreticu
11	318	100.0	417	3	AAY92349 Human MBP
12	318	100.0	417	5	Aau77712 Human cal
13	318	100.0	417	5	Aae24591 Human cal
14	318	100.0	417	5	Aae18851 Human cal
15	318	100.0	417	5	AB282384 Human cal
16	318	100.0	417	6	ABJ19766 Human cal
17	318	100.0	417	6	AG579824 Calreticu
18	318	100.0	417	6	ADA26337 Human cal
19	318	100.0	417	7	ADD22407 HLA-B46 T
20	318	100.0	417	7	Ades6308 Human Pro
21	318	100.0	417	7	Ades6312 Human Pro
22	272	85.5	403	2	AAW04171 Flea calr
23	269	84.6	406	4	AB64414 Drosophil
24	258	81.1	49	3	AAY92353 Recombina
25	242	76.1	336	2	AAI2312 Partial s

26	130	59.7	122	2	AAY00926 Rat cClqR
27	130	59.7	122	2	AAY00924 Human cCl
28	182	57.2	122	2	AAY00925 Mouse cC1
29	177	55.7	415	4	AAB66343 Castor be
30	177	55.7	415	4	AAB66341 Castor be
31	176	55.3	419	7	ABM74155 DNA clone
32	175	55.0	385	3	AB332385 Human sec
33	175	55.0	390	6	ABO07134 Novel hum
34	171	53.8	428	7	ABM74288 DNA Clone
35	170	53.5	420	5	ABB04856 Maize cal
36	169	53.1	312	3	AAg47933 Arabidops
37	169	53.1	312	3	AAg24609 Arabidops
38	169	53.1	332	3	AAg30998 Arabidops
39	169	53.1	421	3	AAg24608 Arabidops
40	169	53.1	421	3	AAg47932 Arabidops
41	169	53.1	424	3	AAg24607 Arabidops
42	169	53.1	424	3	AAg47931 Arabidops
43	169	53.1	441	3	AAg30997 Arabidops
44	169	53.1	444	3	AAg30996 Arabidops
45	117	36.8	592	4	ABB44554 Human wou

ALIGNMENTS

RESULT 1

AAy92354

ID AAY92354 standard; protein; 60 AA.

XX

AC AAY92354;

XX

DT 10-AUG-2000 (first entry)

XX

DE Recombinant human calreticulin residues 121-180.

XX

KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 cytostatic; dermalogical; immunosuppressive; antiinflammatory; hepatic;
 anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

OS Homo sapiens.

OS Synthetic.

XX

PN WO200020577-A1.

XX

PD 13-APR-2000.

XX

PF 05-OCT-1999; 99WO-US023240.

XX

PR 06-OCT-1998; 98US-0103438P.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Tosato G, Pike SE, Yao L;

XX

DR WPI; 2000-303767/26.

XX

PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,

XX

PP useful for suppressing tumor growth.

XX

Claim 4; Page 85; 99pp; English.

XX

CC A novel method of inhibiting endothelial cell growth comprises contacting
 the cells with calreticulin (or its fragments/variants). Fragments of
 calreticulin causes at least 40% inhibition of angiogenesis, tumor growth
 and/or endothelial cell growth (claimed). The method may be used for
 inhibiting angiogenesis in a patient. The angiogenesis is associated with
 a disease other than a tumor that is associated with neovascularization
 (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular
 glaucoma, psoriasis, angiofibromas, immune inflammation,
 atherosclerosis, excessive wound repair, retinal neovascularization,
 macular degeneration, corneal graft rejection, contact lens overwear,
 Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic

CC lupus erythematosus, thyroiditis, Goodpasture's syndrome, systemic
 CC vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary
 CC biliary cirrhosis). The method may also be used for treating/inhibiting
 CC tumor growth especially Kaposi's sarcoma (claimed)
 XX
 SQ Sequence 60 AA;

Query Match 100.0%; Score 318; DB 3; Length 60;
 Best Local Similarity 100.0%; Pred. No. 3e-37;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPQTKKVHVFNYKGNVLINKDIRCKDDEFTHLYTLVLRPNTYEVKIDNSQVESGSLE 60
 |||||
 DB 1 GPQTKKVHVFNYKGNVLINKDIRCKDDEFTHLYTLVLRPNTYEVKIDNSQVESGSLE 60
 |||||

RESULT 2

AA92352
 ID AAY92352 standard; protein; 61 AA.

XX
 AC AAY92352;

XX
 DT 10-AUG-2000 (first entry)

XX
 DE Recombinant human calreticulin residues 120-180.

XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytosolic; dermalogical; immunosuppressive; antinflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

XX Homo sapiens.

OS Synthetic.

XX WO200020577-A1.

PN 13-APR-2000.

XX 05-OCT-1999; 99WO-US023240.

XX 06-OCT-1998; 98US-0103438P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Tosato G, Pike SE, Yao L;

XX WPI; 2000-303767/26.

XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 PT useful for suppressing tumor growth.

XX Claim 4; Page 82-83; 99pp; English.

XX A novel method of inhibiting endothelial cell growth comprises contacting
 CC the cells with calreticulin (or its fragments/variants). Fragments of
 CC calreticulin causes at least 40% inhibition of angiogenesis, tumor growth
 CC and/or endothelial cell growth (claimed). The method may be used for
 CC inhibiting angiogenesis in a patient. The angiogenesis is associated with
 CC a disease other than a tumor that is associated with neovascularization
 CC (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular
 CC glaucoma, psoriasis, angiofibromas, immune inflammation,
 CC atherosclerosis, excessive wound repair, retinal neovascularization,
 CC macular degeneration, corneal graft rejection, contact lens overwear,
 CC Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic
 CC lupus erythematosus, thyroiditis, Goodpasture's syndrome, systemic
 CC vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary
 CC biliary cirrhosis). The method may also be used for treating/inhibiting
 CC tumor growth especially Kaposi's sarcoma (claimed)

XX Sequence 61 AA;

Query Match 100.0%; Score 318; DB 3; Length 61;
 Best Local Similarity 100.0%; Pred. No. 3.1e-37;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPQTKKVHVFNYKGNVLINKDIRCKDDEFTHLYTLVLRPNTYEVKIDNSQVESGSLE 60
 |||||
 DB 2 GPQTKKVHVFNYKGNVLINKDIRCKDDEFTHLYTLVLRPNTYEVKIDNSQVESGSLE 61
 |||||

RESULT 3

AA92351
 ID AAY92351 standard; protein; 180 AA.

XX
 AC AAY92351;

XX 10-AUG-2000 (first entry)

XX Human vasostatin (calreticulin N-terminal 180 amino acids).

XX MBP-calreticulin; maltose binding protein; vasostatin; N-terminal;
 KW angiogenesis; inhibition; endothelial cell; anti-angiogenic;
 KW neuroprotective; antidiabetic; cytosolic; dermalogical; hepatic;
 KW immunosuppressive; antinflammatory; anti-atherosclerotic;
 KW gastrointestinal; anti-arthritis; ophthalmic.

XX Homo sapiens.

OS Synthetic.

XX WO200020577-A1.

XX 13-APR-2000.

XX 05-OCT-1999; 99WO-US023240.

XX 06-OCT-1998; 98US-0103438P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Tosato G, Pike SE, Yao L;

XX WPI; 2000-303767/26.

XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 PT useful for suppressing tumor growth.

XX Claim 4; Page 82; 99pp; English.

XX A novel method of inhibiting endothelial cell growth comprises contacting
 CC the cells with calreticulin (or its fragments/variants). Fragments of
 CC calreticulin causes at least 40% inhibition of angiogenesis, tumor growth
 CC and/or endothelial cell growth (claimed). The method may be used for
 CC inhibiting angiogenesis in a patient. The angiogenesis is associated with
 CC a disease other than a tumor that is associated with neovascularization
 CC (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular
 CC glaucoma, psoriasis, angiofibromas, immune inflammation,
 CC atherosclerosis, excessive wound repair, retinal neovascularization,
 CC macular degeneration, corneal graft rejection, contact lens overwear,
 CC Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic
 CC lupus erythematosus, thyroiditis, Goodpasture's syndrome, systemic
 CC vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary
 CC biliary cirrhosis). The method may also be used for treating/inhibiting
 CC tumor growth especially Kaposi's sarcoma (claimed)

XX Sequence 180 AA;

Query Match 100.0%; Score 318; DB 3; Length 180;

Best Local Similarity 100.0%; Pred. No. 1.2e-36;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPQTKKVHVFNYKGNVLINKDIRCKDDEFTHLYTLVLRPNTYEVKIDNSQVESGSLE 60
 |||||
 DB 121 GPQTKKVHVFNYKGNVLINKDIRCKDDEFTHLYTLVLRPNTYEVKIDNSQVESGSLE 180
 |||||

RESULT 4

AAY92355
 ID AAY92355 standard; protein; 280 AA.
 XX
 AC AAY92355;
 XX
 DT 10-AUG-2000 (first entry)
 XX
 DE Recombinant delta-120 calreticulin.
 XX
 KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermalogical; immunosuppressive; antiinflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX WO200020577-A1.
 XX
 XX 13-APR-2000.
 XX
 XX 05-OCT-1999; 99WO-US023240.
 XX
 XX 06-OCT-1998; 98US-0103438P.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Tosato G, Pike SE, Yao L;
 XX
 XX WPI; 2000-303767/26.
 XX
 XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 XX useful for suppressing tumor growth.
 XX
 XX Claim 4; Page 86; 99pp; English.
 XX
 XX This sequence comprises recombinant human calreticulin (AAY92350) missing
 CC the N-terminal 120 amino acids. A novel method of inhibiting endothelial
 CC cell growth comprises contacting the cells with calreticulin (or its
 CC fragments/variants). Fragments of calreticulin causes at least 40%
 CC inhibition of angiogenesis, tumor growth and/or endothelial cell growth
 CC (claimed). The method may be used for inhibiting angiogenesis in a
 CC patient. The angiogenesis is associated with a disease other than a tumor
 CC that is associated with neovascularization (e.g. diabetic neuropathy,
 CC retrolental fibroplasia, trachoma, neovascular glaucoma, psoriasis,
 CC angiofibromas, immune inflammation, atherosclerosis, excessive wound
 CC repair, retinal neovascularization, macular degeneration, corneal graft
 CC rejection, contact lens overwear, Crohn's disease, non-immune
 CC inflammation, rheumatoid arthritis, systemic lupus erythematosus,
 CC thyroiditis, Goodpasture's syndrome, systemic vasculitis, scleroderma,
 CC Sjorgen's syndrome, sarcoidosis and primary biliary cirrhosis). The
 CC method may also be used for treating/inhibiting tumor growth especially
 CC Kaposi's sarcoma (claimed)
 XX
 XX Sequence 280 AA;
 SQ
 Query Match 100.0%; Score 318; DB 3; Length 280;
 Best Local Similarity 100.0%; Pred. No. 2.2e-36;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPGTKKHVIFNYKGNVLINKDKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 60
 DB 1 GPGTKKHVIFNYKGNVLINKDKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 60
 RESULT 5
 AAY92350
 ID AAY92350 standard; protein; 400 AA.
 XX
 AC AAY92350;
 XX
 XX 10-AUG-2000 (first entry)
 XX
 DE Recombinant human MBP-calreticulin.
 XX
 KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermalogical; immunosuppressive; antiinflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX WO200020577-A1.
 XX
 XX 13-APR-2000.
 XX
 XX 05-OCT-1999; 99WO-US023240.
 XX
 XX 06-OCT-1998; 98US-0103438P.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Tosato G, Pike SE, Yao L;
 XX
 XX WPI; 2000-303767/26.
 XX
 XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 XX useful for suppressing tumor growth.
 XX
 XX Claim 4; Page 86; 99pp; English.
 XX
 XX This sequence comprises recombinant human calreticulin (AAY92350) missing
 CC the N-terminal 120 amino acids. A novel method of inhibiting endothelial
 CC cell growth comprises contacting the cells with calreticulin (or its
 CC fragments/variants). Fragments of calreticulin causes at least 40%
 CC inhibition of angiogenesis, tumor growth and/or endothelial cell growth
 CC (claimed). The method may be used for inhibiting angiogenesis in a
 CC patient. The angiogenesis is associated with a disease other than a tumor
 CC that is associated with neovascularization (e.g. diabetic neuropathy,
 CC retrolental fibroplasia, trachoma, neovascular glaucoma, psoriasis,
 CC angiofibromas, immune inflammation, atherosclerosis, excessive wound
 CC repair, retinal neovascularization, macular degeneration, corneal graft
 CC rejection, contact lens overwear, Crohn's disease, non-immune
 CC inflammation, rheumatoid arthritis, systemic lupus erythematosus,
 CC thyroiditis, Goodpasture's syndrome, systemic vasculitis, scleroderma,
 CC Sjorgen's syndrome, sarcoidosis and primary biliary cirrhosis). The
 CC method may also be used for treating/inhibiting tumor growth especially
 CC Kaposi's sarcoma (claimed)
 XX
 XX Sequence 400 AA;
 SQ
 Query Match 100.0%; Score 318; DB 3; Length 400;
 Best Local Similarity 100.0%; Pred. No. 3.5e-36;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPGTKKHVIFNYKGNVLINKDKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 60
 DB 121 GPGTKKHVIFNYKGNVLINKDKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 180
 RESULT 6
 AAW11156
 ID AAW11156 standard; peptide; 401 AA.
 XX
 AC AAW11156;
 XX
 XX 31-MAY-1997 (first entry)
 XX
 DE Calreticulin.
 DE calreticulin; C-domain; restenosis; inhibitor.
 KW
 KW Homo sapiens.
 OS
 OS WO9636643-A1.
 PN

XX PD 21-NOV-1996.
 XX PF 17-MAY-1996; 96WO-IB000471.
 XX PR 17-MAY-1995; 95US-00442844.
 XX PR 16-MAY-1996; 96US-00649417.
 XX PA (UYAL-) UNIV ALBERTA.
 XX PI Michalak M, Lucas A;
 XX PR WPI; 1997-012036/01.
 XX PR Inhibition of restenosis in patients - using calreticulin or a C-domain polypeptide of calreticulin or a variant with the same activity.
 XX PS Disclosure; Fig 1; 48pp; English.
 XX CC The present sequence is calreticulin. It and a C-domain derived peptide (AAW06736) are useful for treating a patient to inhibit restenosis. The calreticulin-type cpds. are administered either parenterally, CC intravenously or via a catheter and can target areas of vascular damage CC to inhibit or prevent restenosis
 XX SQ Sequence 401 AA;
 Query Match 100.0%; Score 318; DB 2; Length 401;
 Best Local Similarity 100.0%; Pred. No. 3.5e-36;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPGTKVHVIFNYKGNVLINKDIRCKDDEFTHLVTLVLRPNTVEVKIDNSQVSGSLE 60
 Db 121 GPGTKVHVIFNYKGNVLINKDIRCKDDEFTHLVTLVLRPNTVEVKIDNSQVSGSLE 180
 RESULT 7
 ADE56306
 ID ADE56306 standard; protein; 416 AA.
 AC ADE56306;
 XX 29-JAN-2004 (first entry)
 DT Rat Protein P18418, SEQ ID NO 2158.
 DE Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX Rattus norvegicus.
 XX WO2003016475-A2.
 XX 27-FEB-2003.
 XX 14-AUG-2002; 2002WO-US025765.
 XX 14-AUG-2001; 2001US-0312147P.
 XX 01-NOV-2001; 2001US-0346382P.
 XX 26-NOV-2001; 2001US-0333347P.
 XX (GEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 XX GENBANK; P18418.
 XX New composition comprising two or more isolated polypeptides, useful for
 FT preparing a medicament for treating pain in an animal.
 XX Claim 1; Page; 1017pp; English.
 PS

XX CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides; a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 416 AA;
 Query Match 100.0%; Score 318; DB 7; Length 416;
 Best Local Similarity 100.0%; Pred. No. 3.7e-36;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPGTKVHVIFNYKGNVLINKDIRCKDDEFTHLVTLVLRPNTVEVKIDNSQVSGSLE 60
 Db 138 GPGTKVHVIFNYKGNVLINKDIRCKDDEFTHLVTLVLRPNTVEVKIDNSQVSGSLE 197
 RESULT 8
 ADE56310
 ID ADE56310 standard; protein; 416 AA.
 AC ADE56310;
 XX 29-JAN-2004 (first entry)
 DT Rat Protein P18418, SEQ ID NO 2162.
 DE Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX Rattus norvegicus.
 XX WO2003016475-A2.
 XX 27-FEB-2003.
 XX 14-AUG-2002; 2002WO-US025765.
 XX 14-AUG-2001; 2001US-0312147P.
 XX 01-NOV-2001; 2001US-0346382P.
 XX 26-NOV-2001; 2001US-0333347P.
 XX (GEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 XX GENBANK; P18418.
 XX New composition comprising two or more isolated polypeptides, useful for
 FT preparing a medicament for treating pain in an animal.
 XX Claim 1; Page; 1017pp; English.
 PS

PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.

PS Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that
XX modulates its activity is useful for preparing a medicament for treating
XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX therapy). The sequence presented is a rat protein (shown in Table 2 of
XX the specification) which is differentially expressed during pain. Note:
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic form directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 416 AA;

Query Match 100.0%; Score 319; DB 7; Length 416;
Best Local Similarity 100.0%; Pred. No. 3.7e-36;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKVHVIFNYGKGNVLINKDKDEFTHTLTLIVRPDNTYEVKIDNSQVESGSL 60
DB 138 GPGTKKVHVIFNYGKGNVLINKDKDEFTHTLTLIVRPDNTYEVKIDNSQVESGSL 197

RESULT 9

AAP92276
ID AAP92276 standard; protein; 417 AA.

XX AAP92276;

XX 25-MAR-2003 (revised)

XX 23-FEB-1990 (first entry)

XX 60 kD Ro (Ro/SSA) antigen.

XX Sjorens syndrome; systemic lupus erythematosus.

XX Synthetic.

XX WO8909273-A.

XX 05-OCT-1989.

XX 22-MAR-1989; 89WO-US001213.

XX 22-MAR-1988; 88US-00171634.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Sontheimer RD, Lieu TS, Capra JD, Mccaulliffe DP;

XX WPI; 1989-309537/42.

XX N-PSDB; AAP92276.

XX

PT DNA sequences encoding antigenic epitope(s) of RO 60 KD auto-antigen -
PT used in immunoassays to detect rheumatic disease.

PS Disclosure; Fig 2; 88pp; English.

XX Synthetic peptides corresp. to an epitopic core of Ro antigen are
XX expressed recombinantly to detect autoantibodies, for identification of
XX autoimmune diseases. These epitopes are AAs 24-36, 23-36, 188-209, or 241
XX -255. The peptides may be substatd. for ribonucleoprotein particle
XX antigens. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-
XX MAR-2003 to correct PI field.)

XX Sequence 417 AA;

Query Match 100.0%; Score 318; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.7e-36;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKVHVIFNYGKGNVLINKDKDEFTHTLTLIVRPDNTYEVKIDNSQVESGSL 60
DB 138 GPGTKKVHVIFNYGKGNVLINKDKDEFTHTLTLIVRPDNTYEVKIDNSQVESGSL 197

RESULT 10

AAY00927
ID AAY00927 standard; protein; 417 AA.

XX AAY00927;

XX 28-MAY-1999 (first entry)

XX Calreticulin.

XX C1g and collectin receptor; cClqR binding domain; complement ubiquitin;
XX C1g functionality; inhibitor; complement activation; inflammation;
XX myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
XX rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
XX immune complex nephritis; therapy.

XX Homo sapiens.

XX WO9507406-A1.

XX 18-FEB-1999.

XX 12-AUG-1998; 98WO-GB002430.

XX 12-AUG-1997; 97GB-00016998.

XX (UYLE-) UNIV LEICESTER.

XX Schwaeble W;

XX WPI; 1999-180404/15.

XX Use of a cClqR binding domain - to modulate complement ubiquitin (CUB)
XX functionality.

XX Disclosure; Page 26-27; 31pp; English.

XX This sequence is calreticulin, a homologue of C1g and collectin receptor
XX (cClqR). The invention relates to the use of a cClqR binding domain in a
XX medicament to effect complement ubiquitin (CUB) functionality, and an
XX inhibitor of the cClqR binding domain in a medicament to inhibit CUB
XX functionality. The cClqR binding domain, or its inhibitor, can be used to
XX treat a human or animal body. Particularly an inhibitor is used to treat
XX complement activation involved in the initiation and maintenance of
XX inflammation, for example in myocardial infarction, brain ischaemia
XX (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus
XX erythematosus, burns, immune complex nephritis, and to treat amyloid
XX plaques in Alzheimer's disease. The use of cClqR binding domain or
XX inhibitor enables the CUB domain functionality to be modulated using a

CC low molecular weight molecule
XX Sequence 417 AA;
SQ

Query Match 100.0%; Score 318; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.7e-36;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKHVIFNYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 60
DB 138 GPGTKKHVIFNYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 11
AAU77712
ID AAU77712 standard; protein; 417 AA.
XX
AC AAU77712;
XX
DT 05-JUN-2002 (first entry)
XX
DE Human calreticulin (CRT).
XX
KW Calreticulin; CRT; endoplasmic reticulum chaperone polypeptide;
XX
KW cytosolic; vaccine; human papillomavirus 16; HPV 16; E7; DNA vaccine;
XX
KW enhanced antigen-specific immune response; cytotoxic T lymphocyte;
XX
KW tumour; cancer; cervical cancer.
XX
OS Homo sapiens.
XX
PN WO200212281-A2.
XX
PD 14-FEB-2002.
XX
PF 02-AUG-2001; 2001WO-US024134.
XX
PR 03-AUG-2000; 2000US-0222902P.
XX
PS (UYJO) UNIV JOHNS HOPKINS.
XX
PI Wu T, Hung C;
XX
DR WPI; 2002-257463/30.
XX
DR N-PSDB; ABK11662.
XX
PT New nucleic acids encoding a fusion polypeptide comprising an endoplasmic
XX
PT reticulum chaperone polypeptide linked to an antigenic polypeptide,
XX
XX useful as a vaccine for inducing antigen-specific immune responses.
XX
PS Disclosure; Page 27; 71pp; English.
XX
XX The invention describes a nucleic acid molecule (I) encoding a fusion
XX
XX polypeptide comprising a first polypeptide domain comprising an
XX
XX endoplasmic reticulum chaperone polypeptide e.g. calreticulin (CRT) and a
XX
XX second polypeptide domain comprising at least one antigenic peptide e.g.
XX
XX Human papillomavirus 16 (HPV 16) E7. The nucleic acid is useful as a
XX
XX vaccine (DNA vaccine) for inducing enhanced antigen-specific immune
XX
XX responses, particularly those mediated by cytotoxic T lymphocytes. The
XX
XX nucleic acid and compositions comprising the nucleic acid is also useful
XX
XX for inhibiting the growth of tumours and cancers e.g. cervical cancer.
XX
XX This is the amino acid sequence of the human calreticulin (CRT), an
XX
XX endoplasmic reticulum protein used in the creation of a DNA vaccine
XX
XX Sequence 417 AA;
SQ

DT 10-AUG-2000 (first entry)

Human MBP-calreticulin.

MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
cytosolic; dermatological; immunosuppressive; anti-inflammatory; hepatic;
anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

Homo sapiens.

Key Location/Qualifiers

1..17 /label= signal_peptide

18 /label= mature_protein

WO200020577-A1.

13-APR-2000.

05-OCT-1999; 98WO-US023240.

06-OCT-1998; 98US-0103438P.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Tosato G, Pike SE, Yao L;

WPI; 2000-303767/26.

N-PSDB; AAA09346, AAA09347.

Inhibiting endothelial cell growth and angiogenesis using calreticulin,

useful for suppressing tumor growth.

Disclosure; Page 79-80; 99pp; English.

A novel method of inhibiting endothelial cell growth comprises contacting

the cells with calreticulin (or its fragments/variants). Fragments of

calreticulin causes at least 40% inhibition of angiogenesis, tumor growth

and/or endothelial cell growth (claimed). The method may be used for

inhibiting angiogenesis in a patient. The angiogenesis is associated with

a disease other than a tumor that is associated with neovascularization

(e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular

glaucoma, psoriasis, angiofibromas, immune inflammation,

atherosclerosis, excessive wound repair, retinal neovascularization,

macular degeneration, corneal graft rejection, contact lens overwear,

Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic

lupus erythematosus, thyroiditis, Goodpasture's syndrome, systemic

vasculitis, scleroderma, Sjogren's syndrome, sarcoidosis and primary

biliary cirrhosis). The method may also be used for treating/inhibiting

tumor growth especially Kaposi's sarcoma (claimed)

Sequence 417 AA;

SQ

Query Match 100.0%; Score 318; DB 3; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.7e-36;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKHVIFNYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 60
DB 138 GPGTKKHVIFNYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 12
AAU77712
ID AAU77712 standard; protein; 417 AA.
XX
AC AAU77712;
XX
DT 05-JUN-2002 (first entry)
XX
DE Human calreticulin (CRT).
XX
KW Calreticulin; CRT; endoplasmic reticulum chaperone polypeptide;
XX
KW cytosolic; vaccine; human papillomavirus 16; HPV 16; E7; DNA vaccine;
XX
KW enhanced antigen-specific immune response; cytotoxic T lymphocyte;
XX
KW tumour; cancer; cervical cancer.
XX
OS Homo sapiens.
XX
PN WO200212281-A2.
XX
PD 14-FEB-2002.
XX
PF 02-AUG-2001; 2001WO-US024134.
XX
PR 03-AUG-2000; 2000US-0222902P.
XX
PS (UYJO) UNIV JOHNS HOPKINS.
XX
PI Wu T, Hung C;
XX
DR WPI; 2002-257463/30.
XX
DR N-PSDB; ABK11662.
XX
PT New nucleic acids encoding a fusion polypeptide comprising an endoplasmic
XX
PT reticulum chaperone polypeptide linked to an antigenic polypeptide,
XX
XX useful as a vaccine for inducing antigen-specific immune responses.
XX
PS Disclosure; Page 27; 71pp; English.
XX
XX The invention describes a nucleic acid molecule (I) encoding a fusion
XX
XX polypeptide comprising a first polypeptide domain comprising an
XX
XX endoplasmic reticulum chaperone polypeptide e.g. calreticulin (CRT) and a
XX
XX second polypeptide domain comprising at least one antigenic peptide e.g.
XX
XX Human papillomavirus 16 (HPV 16) E7. The nucleic acid is useful as a
XX
XX vaccine (DNA vaccine) for inducing enhanced antigen-specific immune
XX
XX responses, particularly those mediated by cytotoxic T lymphocytes. The
XX
XX nucleic acid and compositions comprising the nucleic acid is also useful
XX
XX for inhibiting the growth of tumours and cancers e.g. cervical cancer.
XX
XX This is the amino acid sequence of the human calreticulin (CRT), an
XX
XX endoplasmic reticulum protein used in the creation of a DNA vaccine
XX
XX Sequence 417 AA;
SQ

AAU77712

AC AAU77712;

DT 05-JUN-2002 (first entry)

DE Human calreticulin (CRT).

KW Calreticulin; CRT; endoplasmic reticulum chaperone polypeptide;

KW cytosolic; vaccine; human papillomavirus 16; HPV 16; E7; DNA vaccine;

KW enhanced antigen-specific immune response; cytotoxic T lymphocyte;

KW tumour; cancer; cervical cancer.

OS Homo sapiens.

PN WO200212281-A2.

PD 14-FEB-2002.

PF 02-AUG-2001; 2001WO-US024134.

PR 03-AUG-2000; 2000US-0222902P.

PS (UYJO) UNIV JOHNS HOPKINS.

PI Wu T, Hung C;

DR WPI; 2002-257463/30.

DR N-PSDB; ABK11662.

PT New nucleic acids encoding a fusion polypeptide comprising an endoplasmic

PT reticulum chaperone polypeptide linked to an antigenic polypeptide,

XX useful as a vaccine for inducing antigen-specific immune responses.

PS Disclosure; Page 27; 71pp; English.

XX The invention describes a nucleic acid molecule (I) encoding a fusion

XX polypeptide comprising a first polypeptide domain comprising an

XX endoplasmic reticulum chaperone polypeptide e.g. calreticulin (CRT) and a

XX second polypeptide domain comprising at least one antigenic peptide e.g.

XX Human papillomavirus 16 (HPV 16) E7. The nucleic acid is useful as a

XX vaccine (DNA vaccine) for inducing enhanced antigen-specific immune

XX responses, particularly those mediated by cytotoxic T lymphocytes. The

XX nucleic acid and compositions comprising the nucleic acid is also useful

XX for inhibiting the growth of tumours and cancers e.g. cervical cancer.

XX This is the amino acid sequence of the human calreticulin (CRT), an

XX endoplasmic reticulum protein used in the creation of a DNA vaccine

XX Sequence 417 AA;
SQ

Query Match 100.0%; Score 318; DB 5; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.7e-36;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKHVIFNYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 60
DB 138 GPGTKKHVIFNYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 13
AAE24591

ID AAE24591 standard; protein; 417 AA.
XX
AC AAE24591;
XX
DT 04-OCT-2002 (first entry)
XX
DE Human calreticulin protein.
XX
KW Human; calreticulin; antisense compound; hyperproliferative disorder;
KW cancer; autoimmune disease; viral infection; cardiovascular disease;
KW antisense therapy; cytostatic; immunosuppressive; virucide.
XX
OS Homo sapiens.
XX
PN WO200236743-A2.
XX
PD 10-MAY-2002.
XX
PF 30-OCT-2001; 2001WO-US049045.
XX
PR 30-OCT-2000; 2000US-00702327.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Cowser LM;
XX
PI WPI; 2002-479759/51.
XX
DR N-PSDB; AAD39469.
XX
XX Novel antisense compound targeted to nucleic acid encoding calreticulin,
PT useful for treating a human having disease or condition associated with
PT calreticulin e.g. cancer, viral infection, autoimmune disease.
XX
PS Disclosure; Page 88-90; 109pp; English.
XX
CC The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of calreticulin. The compositions comprise
CC antisense compounds, particularly antisense oligonucleotides, targeted
CC to nucleic acids encoding calreticulin. The antisense compound is useful
CC for inhibiting the expression of calreticulin in human cells or tissues.
CC It is also useful for treating a human having a disease or condition
CC associated with calreticulin, e.g., hyperproliferative disorder e.g.
CC cancer, autoimmune disease, viral infection or cardiovascular disease, by
CC inhibiting expression of calreticulin. It is useful for diagnostics,
CC therapeutics, prophylaxis and as research reagents and kits. It is also
CC used in antisense therapy. The present sequence is human calreticulin
CC protein. This sequence is used in the exemplification of the invention
XX
SQ Sequence 417 AA;
Query Match 100.0%; Score 318; DB 5; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.7e-36;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GPGTKKHVIFNYKGNVINKDRCCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 60
DB 138 GPGTKKHVIFNYKGNVINKDRCCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 197
RESULT 14
AAE18851
ID AAE18851 standard; protein; 417 AA.
XX
AC AAE18851;
XX
DT 17-MAY-2002 (first entry)
XX
DE Human calreticulin protein.
XX
KW Human; prostate cancer; calreticulin; TID-1 protein; TRAITS protein;
KW androgen action pathway; cell proliferation; kidney cancer; lymphoma;
KW epithelium-derived carcinoma; leukaemia; vaccine; gene therapy;
KW cytostatic; U19 protein.
XX

XX OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT Domain 98..170 /label= N-terminal_domain
FT Region 98..103 /label= Alpha_helix
FT Region 149..154 /label= Alpha_helix
FT Domain 171..285 /note= "Proline-rich domain (P domain)"
FT Domain 286..397 /label= C-terminal_domain
XX
PN WO200206327-A2.
XX
PD 24-JAN-2002.
XX
PF 17-JUL-2001; 2001WO-US022357.
XX
PR 17-JUL-2000; 2000US-0218761P.
PR 16-JUL-2001; 2001US-00906393.
XX
PA (NOUN) UNIV NORTHWESTERN.
XX
XX Wang Z, Xiao W;
XX
XX WPI; 2002-179780/23.
XX
DR N-PSDB; AAD29931.
XX
PT Identifying a subject that is likely to have aggressive form of prostate
PT cancer, involves comparing calreticulin levels in prostate specimen of
PT the subject and in benign prostatic epithelial cells of the same subject.
XX
PS Disclosure; Page 146-148; 149pp; English.
XX
CC The present invention relates to methods of distinguishing aggressive
CC forms of prostate cancer from non-aggressive forms. The method involves
CC comparing the level of calreticulin in prostate specimen and in benign
CC prostatic epithelial cells of a subject. The invention particularly
CC relates to two proteins, namely calreticulin and TID-1 (TRAITS; U19) that
CC are down-regulated in aggressive forms of prostate cancer but not in
CC slowly progressing prostate cancer. They play important roles in the part
CC of androgen action pathway that suppresses cell proliferation and/or
CC prevents prostate cancer. The method is useful for identifying a subject
CC who is likely to have an aggressive form of prostate cancer. The
CC invention further relates to a method of identifying a subject with a
CC slow growing form of prostate cancer. TID-1 sequences are useful for
CC treating cancers such as epithelium-derived carcinomas, kidney cancers,
CC lymphomas, leukaemias and prostate cancers. Sequences of the invention
CC are used as vaccines and in gene therapy. The present sequence is human
CC calreticulin protein
XX
SQ Sequence 417 AA;
Query Match 100.0%; Score 318; DB 5; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.7e-36;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GPGTKKHVIFNYKGNVINKDRCCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 60
DB 138 GPGTKKHVIFNYKGNVINKDRCCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 197
RESULT 15
ABE82384
ID ABE82384 standard; protein; 417 AA.
XX
AC ABE82384;
XX
DT 08-JAN-2003 (first entry)
XX

DE Human calreticulin (CRT) protein.
 XX Immunogenicity; cytostatic; virucide; protozoacide; antibacterial; CTL;
 KW hepatotropic; anti-HIV; vaccine. cytotoxic T lymphocyte; tumour; CRT;
 KW calreticulin; human.
 XX Homo sapiens.
 OS
 XX WO200274920-A2.
 PN
 XX 26-SEP-2002.
 DD
 XX 19-MAR-2002; 2002WO-US008033.
 FF
 XX 16-MAR-2001; 2001US-0276854P.
 PR
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA
 XX Wu T, Hung C;
 PI
 XX WPI; 2002-740856/80.
 DR
 XX N-PSDB; ABV73173.
 DR
 XX New nucleic acid molecule encoding an antigenic fusion polypeptide useful
 PT as vaccines for enhancing or inducing immune responses, primarily
 PT cytotoxic T lymphocytes (CTL) responses to specific antigens such as
 PT tumor or viral antigens.
 XX
 XX Disclosure; Page 27; 93pp; English.
 PS
 XX The invention relates to a nucleic acid molecule that encodes a fusion
 CC polypeptide, comprising a first nucleic acid sequence encoding a
 CC polypeptide that comprises at least one immunogenicity-potentiating
 CC polypeptide, optionally, fused in frame with the nucleic acid, a linker
 CC nucleic acid encoding a linker peptide, and a nucleic acid that is linked
 CC in frame to them, and that encodes an antigenic peptide or polypeptide.
 CC The nucleic acid molecule, polypeptides and vectors are useful as
 CC vaccines for enhancing immune responses, primarily cytotoxic T
 CC lymphocytes (CTL) responses to specific antigens such as tumour or viral
 CC antigens, and for inhibiting growth or preventing re-growth of a tumour.
 CC The packaging cell line is useful for generating alphavirus replicon
 CC particles without contamination from replicon-competent virus. The
 CC pathogenic organisms include viruses such as human papilloma virus (HPV),
 CC hepatitis B virus, hepatitis C virus, human immunodeficiency virus,
 CC Epstein Barr virus and herpes simplex virus, intracellular parasites such
 CC as malaria, and bacteria that grow intracellularly such as mycobacteria
 CC and listeria. The present sequence represents a human calreticulin (CRT)
 XX
 XX Sequence 417 AA;
 SQ
 Query Match 100.0%; Score 318; DB 5; Length 417;
 Best Local Similarity 100.0%; Pred. No. 3.7e-36;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPGTKKHVIFNYKGNVLINKDKCKDETHLYTLIVRPDNTYEVKIDNSQVESGSL 60
 Db 138 GPGTKKHVIFNYKGNVLINKDKCKDETHLYTLIVRPDNTYEVKIDNSQVESGSL 197

Search completed: October 4, 2004, 13:03:31
 Job time : 45.5294 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2004, 13:01:22 ; Search time 13.4118 Seconds
(without alignments)
230.958 Million cell updates/sec

Title: US-09-807-148-8

Perfect score: 318

Sequence: 1 GPGTKVHVIFNYGKGNVLI.....PDNTYEVKIDNSQVSGSLE 60

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
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3: /cgn2_6/ptodata/2/iaa/6A COMB.pcp.*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pcp.*
5: /cgn2_6/ptodata/2/iaa/PTUS COMB.pcp.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	318	100.0	61	4	US-09-828-000-8
2	318	100.0	180	4	US-09-828-000-3
3	318	100.0	416	4	US-09-828-000-2
4	235	73.9	61	4	US-09-828-000-4
5	189	59.4	35	4	US-09-828-000-7
6	177	55.7	415	3	US-08-675-816-2
7	142	44.7	27	4	US-09-828-000-5
8	115	36.2	593	1	US-08-296-362-2
9	107	33.6	610	4	US-09-976-594-947
10	96	30.2	18	4	US-09-828-000-6
11	79	24.8	542	3	US-08-675-816-6
12	61.5	19.3	582	3	US-08-906-865-3
13	61.5	19.3	582	4	US-09-129-668-3
14	57.5	18.1	126	4	US-09-732-210-1163
15	55	17.3	588	4	US-09-252-991A-18861
16	54.5	17.1	410	2	US-08-723-415B-10
17	54.5	17.1	410	3	US-09-189-627A-10
18	54.5	17.1	410	4	US-09-710-861-10
19	54	17.0	405	1	US-07-829-954-2
20	54	17.0	405	1	US-07-994-423-2
21	54	17.0	405	1	US-08-421-891-2
22	54	17.0	474	4	US-09-134-001C-3176
23	54	17.0	816	1	US-08-190-802A-54
24	54	17.0	816	3	US-08-477-346-54
25	54	17.0	816	4	US-08-473-059-54
26	54	17.0	816	4	US-08-487-072A-54
27	54	17.0	1009	4	US-09-693-146-4

Sequence 23, Appl
Sequence 23, Appl
Sequence 6, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 4, Appl
Sequence 3458, Ap
Sequence 9, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 2969, Ap
Sequence 11, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 11, Appl
Sequence 11, Appl

28 53.5 16.8 279 2 US-08-701-191A-23
29 53.5 16.8 279 4 US-09-664-526-23
30 53.5 16.8 355 1 US-08-292-549-6
31 53.5 16.8 355 3 US-09-006-353A-14
32 53.5 16.8 355 4 US-09-573-986-14
33 53.5 16.8 812 1 US-08-446-794A-4
34 53.5 16.8 943 4 US-09-540-236-3458
35 53.5 16.8 984 2 US-08-673-789-9
36 53.5 16.8 984 2 US-08-449-645A-19
37 53.5 16.8 984 2 US-08-702-367A-19
38 53.5 16.8 984 5 FCT-US95-04681-19
39 53 16.7 91 4 US-09-134-001C-2969
40 53 16.7 410 2 US-08-723-415B-11
41 53 16.7 410 2 US-08-428-131-2
42 53 16.7 410 2 US-08-602-846-2
43 53 16.7 410 3 US-09-078-596-2
44 53 16.7 410 3 US-09-189-627A-11
45 53 16.7 410 4 US-09-710-861-11

ALIGNMENTS

RESULT 1
US-09-828-000-8
; Sequence 8, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 8
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Fragment 5
US-09-828-000-8

Query Match 100.0%; Score 318; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 2.1e-36;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKVHVIFNYGKGNVLIKDIRCKDDEFTHTLYLIVRPDNTYEVKIDNSQVSGSLE 60
Db 2 GPGTKVHVIFNYGKGNVLIKDIRCKDDEFTHTLYLIVRPDNTYEVKIDNSQVSGSLE 61

RESULT 2
US-09-828-000-3
; Sequence 3, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Vasostatin
US-09-828-000-3

Query Match 100.0%; Score 318; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 8.6e-36;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKVHVIFNYGKGNVLIKDIRCKDDEFTHTLYLIVRPDNTYEVKIDNSQVSGSLE 60

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Db 121 GPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 180
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RESULT 3
US-09-828-000-2
; Sequence 2, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Calreticulin
US-09-828-000-2
Query Match 100.0%; Score 318; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 2.5e-35;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 60
Db 138 GPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 197
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RESULT 4
US-09-828-000-4
; Sequence 4, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Fragment 1
US-09-828-000-4
Query Match 73.9%; Score 235; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 5.1e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 43
Db 19 GPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 61
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RESULT 5
US-09-828-000-7
; Sequence 7, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 35
; TYPE: PRT
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; ORGANISM: Fragment 4
US-09-828-000-7
Query Match 59.4%; Score 189; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-19;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 43
Db 1 VIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 35
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RESULT 6
US-08-675-816-2
; Sequence 2, Application US/08675816
; Patent No. 6171864
; GENERAL INFORMATION:
; APPLICANT: Coughlan, Sean J.
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 701 Fifth Ave. Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,816
; FILING DATE: 05-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6171864tenburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 750027.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206-622-4900
; TELEFAX: (206)-682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-675-816-2
Query Match 55.7%; Score 177; DB 3; Length 415;
Best Local Similarity 52.5%; Pred. No. 5.3e-16;
Matches 31; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 1 GPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 59
Db 139 GYSTKKVHALNNDTNHLIKKEVPCETDQLTHTYTLIVRPDNTYEVKIDNSQVSGSLE 197
|||||
RESULT 7
US-09-828-000-5
; Sequence 5, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 5
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Fragment 2
US-09-828-000-5

Query Match 44.7%; Score 142; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSGTKKHVIFNYKGNVINKDIRC 26
|||
DB 2 GSGTKKHVIFNYKGNVINKDIRC 27
|||

RESULT 8

US-08-296-362-2
; Sequence 2, Application US/08296362
; Patent No. 5691306
; GENERAL INFORMATION:
; APPLICANT: Bergeron, John J.M.
; APPLICANT: Thomas, David Y.
; APPLICANT: Wada, Ikuo
; TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF
; TITLE OF INVENTION: PROTEIN TRAFFICKING DISORDERS AND INCREASING SECRETORY
; TITLE OF INVENTION: PROTEIN PRODUCTION
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSES: SEED and BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/296,362
; FILING DATE: 25-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deehr, Manva S.
; REGISTRATION NUMBER: 37,120
; REFERENCE/DOCKET NUMBER: 690066.401C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 593 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-296-362-2

Query Match 36.2%; Score 115; DB 1; Length 593;
Best Local Similarity 37.5%; Pred. No. 2.7e-07;
Matches 24; Conservative 12; Mismatches 18; Indels 10; Gaps 1;

QY 6 KHVIFNYKGNVINKDIRC-----DSEFTHLYTLVPRDNTYEVKIDNSQVE 55
|||
DB 200 KLHFIFRHKPKTGVEEKHAKRPDADLKTYFTDKKTHLYTLINPDNSFEILVDQSIYN 259
|||
QY 56 SGSL 59
|||
DB 260 SGSL 263
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RESULT 9

US-09-976-594-947
; Sequence 947, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 947
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 3876162CD1
US-09-976-594-947

Query Match 33.6%; Score 107; DB 4; Length 610;
Best Local Similarity 35.9%; Pred. No. 3.4e-06;
Matches 23; Conservative 11; Mismatches 20; Indels 10; Gaps 1;

QY 6 KHVIFNYKGNVINKDIRC-----DSEFTHLYTLVPRDNTYEVKIDNSQVE 55
|||
DB 190 KLHFIFRHKPKTGVEEKHAKRPDADLKTYFTDKKTHLYTLINPDNSFEILVDQSIYN 249
|||
QY 56 SGSL 59
|||
DB 250 KGSL 253
|||

RESULT 10

US-09-828-000-6
; Sequence 6, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Fragment 3
US-09-828-000-6

Query Match 30.2%; Score 96; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VIFNYKGNVINKDIRC 26
|||
DB 1 VIFNYKGNVINKDIRC 18
|||

RESULT 11

US-08-675-816-6
; Sequence 6, Application US/08675816
; Patent No. 6171864
; GENERAL INFORMATION:
; APPLICANT: Coughlan, Sean J.
; APPLICANT: Winfrey, Jr., Ron J.
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Seed and Berry
 ; STREET: 701 Fifth Ave. Suite 5300
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: U.S.A.
 ; ZIP: 98104-7092
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/675,816
 ; FILING DATE: 05-JUL-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 6171864tenburg, Carol
 ; REGISTRATION NUMBER: 39,317
 ; REFERENCE/DOCKET NUMBER: 750027.401
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206)-622-4900
 ; TELEFAX: (206)-682-6031
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 542 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-675-816-6

 Query Match 24.8%; Score 79; DB 3; Length 542;
 Best Local Similarity 30.2%; Pred. No. 0.02;
 Matches 19; Conservative 10; Mismatches 24; Indels 10; Gaps 3;

 QY 1 GP-----GKVKVHTFNVKG--KNVLINKDIR----CKDBEFTHLYTLIVRPDNTYEVKID 50
 DB 143 GPDCKGATNKVHFILKHKPKSGEYIEHLLKYPSPVSKLTHVYTAILKPDNEURLIIVD 202

 QY 51 NSQ 53
 DB 203 GEE 205

 RESULT 12
 US-08-906-865-3
 ; Sequence 3, Application US/08906865
 ; Patent No. 6040168
 ; GENERAL INFORMATION:
 ; APPLICANT: Greengard, Paul
 ; APPLICANT: Porton, Barbara
 ; APPLICANT: Kao, Hung-Teh
 ; TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE
 ; TITLE OF INVENTION: AND USES THEREOF
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: David A. Jackson, Esq.
 ; STREET: 411 Hackensack Ave, Continental Plaza, 4th
 ; STREET: Floor
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/906,865
 ; FILING DATE:
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.

; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 600-1-202
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-487-5800
 ; TELEFAX: 201-343-1684
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 582 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; DESCRIPTION: /desc = "Synapsin IIA"
 ; HYPOTHETICAL: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 ; US-08-906-865-3

 Query Match 19.3%; Score 61.5; DB 3; Length 582;
 Best Local Similarity 40.0%; Pred. No. 5.6;
 Matches 14; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

 QY 13 YKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEV 47
 DB 130 FRGKKVLGDYDIKVEQAEFSEL-NLVAHADGTYAV 163

 RESULT 13
 US-09-129-668-3
 ; Sequence 3, Application US/09129668B
 ; Patent No. 6429010
 ; GENERAL INFORMATION:
 ; APPLICANT: Greengard, Paul
 ; APPLICANT: Porton, Barbara
 ; APPLICANT: Kao, Hung-Teh
 ; TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: 600-1-202 CIP
 ; CURRENT APPLICATION NUMBER: US/09/129,668B
 ; CURRENT FILING DATE: 1998-08-05
 ; EARLIER APPLICATION NUMBER: 08/906,865
 ; EARLIER FILING DATE: 1997-08-06
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 582
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-129-668-3

 Query Match 19.3%; Score 61.5; DB 4; Length 582;
 Best Local Similarity 40.0%; Pred. No. 5.6;
 Matches 14; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

 QY 13 YKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEV 47
 DB 130 FRGKKVLGDYDIKVEQAEFSEL-NLVAHADGTYAV 163

 RESULT 14
 US-09-732-210-1163
 ; Sequence 1163, Application US/09732210
 ; Patent No. 6573361
 ; GENERAL INFORMATION:
 ; APPLICANT: Bunkers, Greg J.
 ; APPLICANT: Liang, Jihong
 ; APPLICANT: Mittanek, Cindy A.
 ; APPLICANT: Seale, Jeffrey W.
 ; APPLICANT: Wu, Yennie S.
 ; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
 ; FILE REFERENCE: 38-21(15036)B
 ; CURRENT APPLICATION NUMBER: US/09/732,210
 ; CURRENT FILING DATE: 2000-12-07

; PRIOR APPLICATION NUMBER: US 60/169,513
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: US 60/169,340
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 1753
; SEQ ID NO 1163
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Porphyra purpurea
US-09-732-210-1163

Query Match 18.1%; Score 57.5; DB 4; Length 126;
Best Local Similarity 21.9%; Pred. No. 2.8;
Matches 16; Conservative 20; Mismatches 20; Indels 17; Gaps 4;

QY 2 PGTKKVHVFN-----KGNVL-----INKDIRCK---DDEFTHTLYTLIVRPDNTYEV 47
DB 10 PANKREIALTYIGILSRSEILKTKTNIDIRCONLNDOQIVSIREIL---ESSYQI 65

QY 48 KIDNSQVBSGLE 60
DB 67 EGDKKRFESMSIK 79

RESULT 15

US-09-252-991A-18861
; Sequence 18861, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18861
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18861

Query Match 17.3%; Score 55; DB 4; Length 588;
Best Local Similarity 48.0%; Pred. No. 44;
Matches 12; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 14 KGNVLINKDIRCKDDEFTHTLYTLI 38
DB 364 RGGDPLLGKDIRKLDVDDVDTAI 388

Search completed: October 4, 2004, 13:07:21
Job time : 14.4116 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2004, 13:06:03 ; Search time 44.1176 Seconds
(without alignments)
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Title:
Perfect score: 318
Sequence: 1 GPCTKKVHVFYFKYGNVLI.....PDNTVEVKIDNSQVSGSLE 60

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Gapop 10.0 , Gapext 0.5

Searched: 1351062 segs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	318	100.0	61	15	US-10-405-588-8
3	318	100.0	180	10	US-09-828-000-3
4	318	100.0	180	15	US-10-405-588-3
5	318	100.0	416	10	US-09-828-000-2
6	318	100.0	416	14	US-10-316-253-2
7	318	100.0	416	14	US-10-316-253-4
8	318	100.0	416	14	US-10-316-253-6
9	318	100.0	416	15	US-10-405-588-2
10	318	100.0	417	10	US-09-906-393A-36
11	318	100.0	417	14	US-10-161-959-29
12	318	100.0	417	15	US-10-367-093-14
13	235	73.9	61	10	US-09-828-000-4
14	235	73.9	61	15	US-10-405-588-4
15	210.5	66.2	395	15	US-10-369-493-6343

US-09-807-148-8

Sequence: 318

Sequence: 1 GPCTKKVHVFYFKYGNVLI.....PDNTVEVKIDNSQVSGSLE 60

Scoring table: BLOSUM62

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Searched: 1351062 segs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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US-09-828-000-8

Sequence 8, Application US/09828000

Publication No. US20030078198A1

GENERAL INFORMATION:

APPLICANT: Government of the United States of America

TITLE OF INVENTION: Vasostatin as Marrow Protectant

FILE REFERENCE: 4239-55414

CURRENT APPLICATION NUMBER: US/09/828,000

CURRENT FILING DATE: 2001-04-06

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn version 3.0

SEQ ID NO 8

LENGTH: 61

TYPE: PRT

ORGANISM: Fragment 5

US-09-828-000-8

Query Match 100.0%; Score 318; DB 10; Length 61;

Best Local Similarity 100.0%; Pred. No. 1.5e-34;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 2 GPCTKKVHVFYFKYGNVLI.....PDNTVEVKIDNSQVSGSLE 61

RESULT 2

US-10-405-588-8

Sequence 8, Application US/10405588

Publication No. US20030216299A1

GENERAL INFORMATION:

APPLICANT: Government of the United States of America

TITLE OF INVENTION: Vasostatin as Marrow Protectant

FILE REFERENCE: 4239-55414

CURRENT APPLICATION NUMBER: US/10/405,588

CURRENT FILING DATE: 2003-04-01

PRIOR APPLICATION NUMBER: US/09/828,000

US-10-405-588-8

Sequence 8, Appli

Sequence 8, Appli

Sequence 3, Appli

Sequence 3, Appli

Sequence 2, Appli

Sequence 2, Appli

Sequence 6, Appli

Sequence 2, Appli

Sequence 36, Appli

Sequence 29, Appli

Sequence 14, Appli

Sequence 4, Appli

Sequence 4, Appli

Sequence 6343, Ap

US-09-828-000-8

Sequence 8, Application US/09828000

Publication No. US20030078198A1

GENERAL INFORMATION:

APPLICANT: Government of the United States of America

TITLE OF INVENTION: Vasostatin as Marrow Protectant

FILE REFERENCE: 4239-55414

CURRENT APPLICATION NUMBER: US/09/828,000

CURRENT FILING DATE: 2001-04-06

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn version 3.0

SEQ ID NO 8

LENGTH: 61

TYPE: PRT

ORGANISM: Fragment 5

US-09-828-000-8

Query Match 100.0%; Score 318; DB 10; Length 61;

Best Local Similarity 100.0%; Pred. No. 1.5e-34;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPCTKKVHVFYFKYGNVLI.....PDNTVEVKIDNSQVSGSLE 60

DB 2 GPCTKKVHVFYFKYGNVLI.....PDNTVEVKIDNSQVSGSLE 61

RESULT 2

US-10-405-588-8

Sequence 8, Application US/10405588

Publication No. US20030216299A1

GENERAL INFORMATION:

APPLICANT: Government of the United States of America

TITLE OF INVENTION: Vasostatin as Marrow Protectant

FILE REFERENCE: 4239-55414

CURRENT APPLICATION NUMBER: US/10/405,588

CURRENT FILING DATE: 2003-04-01

PRIOR APPLICATION NUMBER: US/09/828,000

US-10-405-588-8

Sequence 8, Appli

Sequence 8, Appli

Sequence 3, Appli

Sequence 3, Appli

Sequence 2, Appli

Sequence 2, Appli

Sequence 6, Appli

Sequence 2, Appli

Sequence 36, Appli

Sequence 29, Appli

Sequence 14, Appli

Sequence 4, Appli

Sequence 4, Appli

Sequence 6343, Ap

US-09-828-000-8

Sequence 8, Application US/09828000

Publication No. US20030078198A1

GENERAL INFORMATION:

APPLICANT: Government of the United States of America

TITLE OF INVENTION: Vasostatin as Marrow Protectant

FILE REFERENCE: 4239-55414

CURRENT APPLICATION NUMBER: US/09/828,000

CURRENT FILING DATE: 2001-04-06

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn version 3.0

SEQ ID NO 8

LENGTH: 61

TYPE: PRT

ORGANISM: Fragment 5

US-09-828-000-8

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Best Local Similarity 100.0%; Pred. No. 1.5e-34;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-10-405-588-8

Sequence 8, Application US/10405588

Publication No. US20030216299A1

GENERAL INFORMATION:

APPLICANT: Government of the United States of America

TITLE OF INVENTION: Vasostatin as Marrow Protectant

FILE REFERENCE: 4239-55414

CURRENT APPLICATION NUMBER: US/10/405,588

CURRENT FILING DATE: 2003-04-01

PRIOR APPLICATION NUMBER: US/09/828,000

US-10-405-588-8

Sequence 8, Appli

Sequence 8, Appli

Sequence 3, Appli

Sequence 3, Appli

Sequence 2, Appli

Sequence 2, Appli

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Sequence 2, Appli

Sequence 36, Appli

Sequence 29, Appli

Sequence 14, Appli

Sequence 4, Appli

Sequence 4, Appli

Sequence 6343, Ap

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; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
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; LENGTH: 61
; TYPE: PRT
; ORGANISM: Fragment 5
US-10-405-588-8

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RESULT 3
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; Sequence 3, Application US/09828000
; Publication No. US20030078198A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Vasostatin
US-09-828-000-3

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Best Local Similarity 100.0%; Pred. No. 6.1e-34;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 180

RESULT 4
US-10-405-588-3
; Sequence 3, Application US/10405588
; Publication No. US20030216299A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/10/405,588
; PRIOR FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US/09/828,000
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Vasostatin
US-10-405-588-3

Query Match      100.0%; Score 318; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 6.1e-34;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
US-09-828-000-2
; Sequence 2, Application US/09828000
; Publication No. US20030078198A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Calcitriculin
US-09-828-000-2

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Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
US-10-316-253-2
; Sequence 2, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-2

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US-10-316-253-4
; Sequence 4, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
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; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 416
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; ORGANISM: Rattus norvegicus
US-10-316-253-4

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US-10-316-253-6
; Sequence 6, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
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; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-6

Query Match      100.0%; Score 318; DB 14; Length 416;
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; Sequence 2, Application US/10405588
; Publication No. US20030216299A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/10/405,588
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US/09/828,000
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.0
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; ORGANISM: Calreticulin
US-10-405-588-2
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US-09-906-393A-36
; Sequence 36, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 36
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-393A-36

Query Match      100.0%; Score 318; DB 10; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 60
Db 138 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 197

RESULT 11
US-10-161-959-29
; Sequence 29, Application US/10161959
; Publication No. US20030096748A1
; GENERAL INFORMATION:
; APPLICANT: Holoshitz, Joseph
; APPLICANT: Ling, Song
; TITLE OF INVENTION: Methods and Compositions for the Treatment of Diseases Associated with Signal Transduction Aberrations
; FILE REFERENCE: UM-07135
; CURRENT APPLICATION NUMBER: US/10/161,959
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/295,691
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 29
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-161-959-29

Query Match      100.0%; Score 318; DB 14; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 60
Db 138 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 197
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RESULT 12
US-10-367-093-14
; Sequence 14, Application US/10367093
; Publication No. US20030216315A1
; GENERAL INFORMATION:
; APPLICANT: Duke University
; APPLICANT: Nicchitta, Chris
; APPLICANT: Baker-LePain, Julie
; TITLE OF INVENTION: MODULATION OF IMMUNE RESPONSE BY NON-PEPTIDE BINDING STRESS RESPON
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 180/145
; CURRENT APPLICATION NUMBER: US/10/367,093
; CURRENT FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-093-14

Query Match      73.9%; Score 318; DB 15; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKVHVIENYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 60
Db 138 GPGTKKVHVIENYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 13
US-09-828-000-4
; Sequence 4, Application US/09828000
; Publication No. US20030078198A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; FILE REFERENCE: Vascostatin as Marrow Protectant
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Fragment 1
US-09-828-000-4

Query Match      73.9%; Score 235; DB 10; Length 61;
Best Local Similarity 100.0%; Pred. No. 1.6e-23;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKVHVIENYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 43
Db 19 GPGTKKVHVIENYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 61

RESULT 14
US-10-405-588-4
; Sequence 4, Application US/10405588
; Publication No. US20030216299A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; FILE REFERENCE: Vascostatin as Marrow Protectant
; CURRENT APPLICATION NUMBER: US/10/405,588
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US/09/828,000
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 61
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; TYPE: PRT
; ORGANISM: Fragment 1
US-10-405-588-4

Query Match      73.9%; Score 235; DB 15; Length 61;
Best Local Similarity 100.0%; Pred. No. 1.6e-23;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKVHVIENYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 60
Db 19 GPGTKKVHVIENYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 192

RESULT 15
US-10-369-493-6343
; Sequence 6343, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6343
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6343

Query Match      66.2%; Score 210.5; DB 15; Length 395;
Best Local Similarity 66.7%; Pred. No. 3.1e-19;
Matches 40; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

QY 1 GPGTKKVHVIENYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 60
Db 134 GP-TRRVHVLNKGKGNLKIETCKSDDELTHLYTLINSDNTYEVKIDGESAQTSLE 192

Search completed: October 4, 2004, 13:17:34
Job time : 45.1176 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2004, 12:55:52 ; Search time 13.0588 Seconds
(without alignments)
441.961 Million cell updates/sec

Title: US-09-807-148-8

Perfect score: 318

Sequence: 1 GPQTKVHVIFNYKGNVL.....PDNTYEVKIDNSQVSGSLE 60

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR:78:*

2: PIR:1:*

3: PIR:3:*

4: PIR:4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	318	100.0	416	1 S06763	calreticulin precu
2	318	100.0	416	2 JH0819	calreticulin precu
3	318	100.0	417	1 A37047	calreticulin precu
4	318	100.0	418	1 A34154	calreticulin precu
5	313	98.4	400	2 S43376	calreticulin, brai
6	313	98.4	421	2 S36799	calreticulin precu
7	281	88.4	405	1 JH0795	calreticulin (clon
8	278	87.4	384	2 S29130	calreticulin precu
9	278	87.4	411	2 S29129	calreticulin homol
10	269	84.6	406	2 A56637	calreticulin precu
11	262	82.4	419	2 S71343	calreticulin precu
12	242	76.1	336	2 A32507	41K larval antigen
13	227	71.4	393	1 A48573	calreticulin autoa
14	210.5	66.2	395	2 S25811	calreticulin precu
15	184	57.9	416	2 T44554	calreticulin - bee
16	179	56.3	421	2 S58170	calreticulin precu
17	177	55.7	415	2 T10172	calreticulin - cas
18	176	55.3	412	2 T05703	calreticulin - bar
19	176	55.3	415	2 T05705	calreticulin - bar
20	172	54.1	425	2 C36605	calreticulin (Crt1
21	169	53.1	389	2 T03691	calreticulin - com
22	169	53.1	416	2 T16968	calreticulin cali
23	169	53.1	444	2 H86224	hypothetical prote
24	168	52.8	422	2 T07841	probable calreticu
25	117	36.8	592	2 I53260	calnexin - human
26	117	36.8	592	2 A46673	calnexin precursor
27	116	36.5	591	2 B54354	calnexin precursor
28	116	36.5	591	2 C54354	calnexin precursor
29	115	36.2	593	1 A37273	calnexin precursor

ALIGNMENTS

RESULT 1

S06763

calreticulin precursor - mouse

N:Alternate names: 55K calcium-binding reticuloplasmin; calregulin

C:Species: Mus musculus (house mouse)

C:Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S06763; JCI1444; FCI233; A57498

R:Smith, M.J.; Koch, G.L.E.

EMBO J. 8, 3581-3586, 1989

A:Title: Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a m

A:Reference number: S06763; MUID:90059955; PMID:2583110

A:Accession: S06763

A:Molecule type: DNA

A:Residues: 1-416 <SMI>

A:Cross-references: EMBL:X14926; NID:G50567; PIDN:CAA33053.1; PID:G50568

R:Mazzarella, R.A.; Gold, P.; Cunningham, M.; Green, M.

Gene 120, 217-225, 1992

A:Title: Determination of the sequence of an expressible cDNA clone encoding ERp60/calr

A:Reference number: JCI1444; MUID:93013037; PMID:1398135

A:Accession: JCI1444

A:Molecule type: mRNA

A:Residues: 1-416 <MAZ>

A:Cross-references: GB:I92988; NID:G193084; PIDN:AAA37569.1; PID:G193085

A:Accession: PCI233

A:Molecule type: protein

A:Residues: 18-41 <MA2>

R:White, T.K.; Zhu, Q.; Tanzer, M.L.

J. Biol. Chem. 270, 15926-15929, 1995

A:Title: Cell surface calreticulin is a putative mannoside lectin which triggers mouse

A:Reference number: A57498; MUID:95332280; PMID:7608143

A:Accession: A57498

A>Status: preliminary

A:Molecule type: Protein

A:Residues: 74-80;142-151;186-193 <WHI>

C:Superfamily: calreticulin

C:Keywords: calcium binding

P:1-17/Domain: signal sequence #status predicted <SIG>

F:18-416/Product: calregulin #status experimental <MAT>

F:413-416/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 318; DB 1; Length 416;

Best Local Similarity 100.0%; Pred. No. 6.2e-30;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPQTKVHVIFNYKGNVLINIKDKDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 60

Db 138 GPQTKVHVIFNYKGNVLINIKDKDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 2

JH0819

calreticulin precursor - rat

N;Alternate names: calcium-binding protein 3
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence revision 20-Aug-1994 #text change 20-Jun-2000
C;Accession: JH0819; A49176; S11205; PC1109; S45036; S04867; S39372; A34473; S13045
R;Nakamura, M.; Moriya, M.; Baba, T.; Michikawa, Y.; Yamanobe, T.; Arai, K.; Okinaga, S.;
Exp. Cell Res. 205 101-110, 1993
A;Title: An endoplasmic reticulum protein, calreticulin, is transported into the acrosom
A;Reference number: A49176; MUID:93202172; PMID:8453984
A;Accession: JH0819
A;Molecule type: mRNA
A;Residues: 1-416 <NAK>
A;Cross-references: GB:D78308; NID:g1089798; PIDN:BAA11345.1; PID:g1845572
A;Accession: A49176
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-416 <NA2>
A;Cross-references: GB:D78308; NID:g1089798; PIDN:BAA11345.1; PID:g1845572
A;Experimental source: Sprague-Dawley, spermatogenic cells
A;Note: sequence extracted from NCBI backbone (NCBIN:127639, NCBI:P.127643)
R;Murthy, K.K.; Banville, D.; Srikant, C.B.; Carrier, F.; Holmes, C.; Bell, A.; Patel, Y.;
Nucleic Acids Res. 18, 4933, 1990
A;Title: Structural homology between the rat calreticulin gene product and the Onchocerc
A;Reference number: S11205; MUID:90370496; PMID:2395661
A;Accession: S11205
A;Molecule type: mRNA
A;Residues: 1-416 <MUR>
A;Cross-references: EMBL:X53363; NID:q55954; PIDN:CAA37446.1; PID:g55855
R;Nakamura, M.; Michikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.
Biochem. Biophys. Res. Commun. 186, 668-673, 1992
A;Title: Calreticulin is present in the acrosome of spermatids of rat testis.
A;Reference number: PC1109; MUID:92360010; PMID:1497655
A;Accession: PC1109
A;Molecule type: protein
A;Residues: 18-32 <NAK2>
A;Experimental source: testis, strain Sprague-Dawley
R;Soennichsen, B.; Fuellekrug, J.; van Nguyen, P.; Diekmann, W.; Robinson, D.G.; Mieskes
submitted to the EMBL Data Library, May 1994
A;Description: Retention and retrieval: both mechanisms cooperate to maintain calreticul
A;Reference number: S45036
A;Accession: S45036
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-416 <SBE>
A;Cross-references: EMBL:Y93327; NID:g488840; PIDN:CAA55890.1; PID:g488841
R;Lone, Y.C.; Bailly, A.; Latruffe, N.
submitted to the EMBL Data Library, December 1988
A;Reference number: S04867
A;Accession: S04867
A;Molecule type: mRNA
A;Residues: 'R', 270-358, 'AAG' <LON>
A;Cross-references: EMBL:X13702; NID:g56055; PIDN:CAA31987.1; PID:g930260
A;Note: the authors designated the protein as D-beta-hydroxybutyrate dehydrogenase
R;Yokoi, T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horiuchi, R.; Kamataki, T.
Biochim. Biophys. Acta 1158, 339-344, 1993
A;Title: Identification of protein disulfide isomerase and calreticulin as autoimmune an
A;Reference number: S39371; MUID:94072621; PMID:8251535
A;Accession: S39372
A;Molecule type: protein
A;Residues: 18-23, 'X', 25-32 <YOK>
R;Van, P.N.; Peter, F.; Soeling, H.D.
J. Biol. Chem. 264, 17494-17501, 1989
A;Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes wit
itive calcium sequestering rat liver vesicles.
A;Reference number: A34473; MUID:90008920; PMID:2793869
A;Accession: A34473
A;Status: preliminary
A;Molecule type: protein
A;Residues: 18-36 <VAN>
R;Treves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meld
Biochem. J. 271, 473-480, 1990
A;Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage
A;Reference number: S13045; MUID:91054414; PMID:2241926
A;Accession: S13045

A:Molecule type: protein
A:Residues: 18-29 <TRE>
C:Superfamily: calreticulin
C:Keywords: calcium binding; glycoprotein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-416/Product: calreticulin #status experimental <NAT>
F:204-412/Region: nuclear location signal
F:443-416/Region: endoplasmic reticulum retention signal
F:344/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 318; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. No. 6,2.e-30; Indels 0; Gaps 0;
Matches 60; Conservative 0; Mismatches 0;

Qy 1 GPGTKKHVIFNYKGNVLINKDIRCKDDFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 60
|||||
Db 138 GPGTKKHVIFNYKGNVLINKDIRCKDDFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 3
A37047
calreticulin precursor - human
N:Alternate names: 52K ribonucleoprotein autoantigen Ro/SS-A; 60K integrin-binding protein
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 18-Feb-2000
C:Accession: A42330; A37047; A46452; A28812; PH1525; A40346; S11475; T45075
R:McCaulliffe, D.P.; Yang, Y.S.; Wilson, J.; Sontheimer, R.D.; Capra, J.D.
J. Biol. Chem. 267, 2557-2562, 1992
A:Title: The 5'-flanking region of the human calreticulin gene shares homology with the
A:Reference number: A42330; MUID:92129342; PMID:1733953
A:Accession: A42330
A:Molecule type: DNA
A:Residues: 1-417 <MC2>
A:Note: sequence extracted from NCBI backbone (NCBIN:78537, NCBI:78536)
R:McCaulliffe, D.P.; Lux, F.A.; Lieu, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachinski
J. Clin. Invest. 85, 1379-1391, 1990
A:Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/SS-A
A:Reference number: A37047; MUID:90237213; PMID:2332496
A:Accession: A37047
A:Molecule type: mRNA
A:Residues: 1-417 <MCC>
A:Cross-references: GB:M32294; NID:g337486; PIDN:AAA36582.1; PID:g337487
A:Note: the authors translated the codon GTA for residue 349 as Tyr
R:Rocheach, L.A.; Haselby, J.A.; Meilof, J.F.; Smeenk, R.J.; Unnasch, T.R.; Greene, B.M.;
J. Immunol. 147, 3031-3039, 1991
A:Title: Characterization of the autoantigen calreticulin.
A:Reference number: A46452; MUID:92013129; PMID:1919005
A:Accession: A46452
A:Molecule type: mRNA
A:Residues: 1-417 <ROR>
A:Cross-references: GB:M44739; NID:g179881; PIDN:AAA51916.1; PID:g179882
A:Note: sequence extracted from NCBI backbone (NCBIN:60749, NCBI:60750)
R:Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sontheimer, R.D.
J. Clin. Invest. 82, 96-101, 1988
A:Title: Molecular characterization of human Ro/SS-A antigen. Amino terminal sequence of
A:Reference number: A28812; MUID:88273610; PMID:3260607
A:Accession: A28812
A:Molecule type: protein
A:Residues: 18-41 <LIE>
A:Note: 18-Ala was also found
R:Dupuis, M.; Schaefer, E.; Krause, K.H.; Tschopp, J.
J. Exp. Med. 177, 1-7, 1993
A:Title: The calcium-binding protein calreticulin is a major constituent of lytic granu-
A:Reference number: PH1525; MUID:93115648; PMID:8418194
A:Accession: PH1525
A:Molecule type: protein
A:Residues: 18-27 <DUP>
A:Experimental source: LAK cell
R:Rojiani, M.V.; Finlay, B.B.; Gray, V.; Dedhar, S.
Biochemistry 30, 9859-9866, 1991
A:Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (cal-
A:Reference number: A40346; MUID:92002034; PMID:1911778
A:Accession: A40346

Db 138 GPGTKKVVFNFKGKNVINKIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSL 197

RESULT 5

S43376

calreticulin, brain isoform 1 - bovine

C;Species: Bos primigenius taurus (cattle)

C;date: 20-Oct-1994 #sequence_revision 23-Mar-1995 #text_change 07-May-1999

C;Accession: S43376; S36801

R;Matsuoka, K.; Seta, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isobe, T.

Biochem. J. 298, 435-442, 1994

A;Title: Covalent structure of bovine brain calreticulin.

A;Reference number: S43376; MUID:94183174; PMID:8135753

A;Accession: S43376

A;Molecule type: protein

A;Residues: 1-400 <MAT>

A;Experimental source: brain

R;Liu, N.; Fine, R.E.; Johnson, R.J.

Biochim. Biophys. Acta 1202, 70-76, 1993

A;Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin

A;Reference number: S36799; MUID:93385184; PMID:8373827

A;Accession: S36801

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 45-63, 'E', '65-83 <LIU>

A;Experimental source: brain, clone 8.1

C;Superfamily: calreticulin

C;Keywords: calcium binding; glycoprotein

F;397-400/Region: endoplasmic reticulum retention signal

F;120-146/Disulfide bonds: #status experimental

F;162/Binding site: carbohydrate (Asn) #status experimental

Query Match 98.4%; Score 313; DB 2; Length 400;

Best Local Similarity 98.3%; Pred. No. 2.3e-29;

Matches 59; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPGTKKVVFNFKGKNVINKIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSL 60

121 GPGTKKVVFNFKGKNVINKIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSL 180

Db

RESULT 6

S36799

calreticulin precursor, brain isoform 2 - bovine

C;Species: Bos primigenius taurus (cattle)

C;date: 10-Dec-1993 #sequence_revision 23-Mar-1995 #text_change 13-Aug-1999

C;Accession: S36799; S36800

R;Liu, N.; Fine, R.E.; Johnson, R.J.

Biochim. Biophys. Acta 1202, 70-76, 1993

A;Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin

A;Reference number: S36799; MUID:93385184; PMID:8373827

A;Accession: S36799

A;Molecule type: mRNA

A;Residues: 1-421 <LIU>

A;Cross-references: GB:LI3462; NID:9348693; PIDN:AAC37307.1; PID:9348694

A;Experimental source: brain, clone 9.4

A;Accession: S36800

A;Molecule type: protein

A;Residues: 35-45 <LI2>

C;Superfamily: calreticulin

C;Keywords: calcium binding; glycoprotein

F;1-34/Domain: signal sequence #status predicted <SIG>

F;35-421/Product: calreticulin, brain isoform 2 #status predicted <MAT>

F;418-421/Region: endoplasmic reticulum retention signal

F;141-167/Disulfide bonds: #status predicted

F;183/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	98.4%;	Score 313;	DB 2;	Length 421;
Best Local Similarity	98.3%;	Pred. No. 2.5e-29;		
Matches	59;	Conservative	1;	Mismatches 0;
				Indels 0;
				Gaps 0;

QV 1 GPGTKKVHVIENYKGKQVLINKDIRCKDDEFTHLYTLVRPDNTYEVKIDNSQVESGSLE 60

Db 142 GPGTKVHVIFNYKGNVLINKDIRCKDDFTHTLYTLVRPNTYEVKIDNSQVSGSLE 201
 |||||

RESULT 7

JH0795
 calreticulin precursor - California sea hare
 N:Alternate names: protein 407
 C:Species: Aplysia californica (California sea hare)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: JH0795; B31409; F60977
 R:Kennedy, T.E.; Kuhl, D.; Barzilai, A.; Sweatt, J.D.; Kandel, E.R.
 Neuron 9, 1013-1024, 1992
 A:Title: Long-term sensitization training in aplysia leads to an increase in calreticulin
 A:Reference number: JH0795; PMID:93098937; PMID:1463604
 A:Accession: JH0795
 A:Molecule type: mRNA
 A:Residues: 1-405 <KEN>
 A:Cross-references: GB:951239; NID:9262053; PIDN:BA24569.1; PID:9262054
 A:Experimental source: abdominal ganglion and antral nervous system
 R:Kennedy, T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, E.R.; Sweatt, J.D.
 Proc. Natl. Acad. Sci. U.S.A. 85, 7008-7012, 1988
 A:Title: Sequencing of proteins from two-dimensional gels by using in situ digestion and
 tion in Aplysia.
 A:Reference number: A94207; PMID:88320566; PMID:3413132
 A:Accession: B31409
 A:Molecule type: protein
 A:Residues: 'X', 17-28, 'X', 30-31 <KE2>
 R:Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl, K.
 Electrophoresis 10, 152-157, 1989
 A:Title: Development of a database of amino acid sequences for proteins identified and i
 A:Reference number: A60977; PMID:89276264; PMID:2731514
 A:Accession: F60977
 A:Molecule type: protein
 A:Residues: 'X', 17-28, 'X', 30-31 <SWE>
 C:Superfamily: calreticulin
 C:Keywords: calcium binding; endoplasmic reticulum
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:16-405/Product: calreticulin #status experimental <MAT>
 F:402-405/Region: endoplasmic reticulum retention signal

Query Match 88.4%; Score 281; DB 1; Length 405;
 Best Local Similarity 85.0%; Pred. No. 15e-25;
 Matches 51; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 GPGTKVHVIFNYKGNVLINKDIRCKDDFTHTLYTLVRPNTYEVKIDNSQVSGSLE 60
 |||||

Db 134 GPGTKVHVIFNYKGNVLINKDIRCKDDFTHTLYTLVRPNTYEVKIDNSQVSGSLE 193
 |||||

RESULT 8

S29130
 calreticulin (clone 8) - African clawed frog (fragment)
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
 C:Accession: S29130; T01068
 R:Traves, S.; Zorzato, F.; Pozzan, T.
 Biochem. J. 287, 579-581, 1992
 A:Title: Identification of calreticulin isoforms in the central nervous system.
 A:Reference number: S29129; PMID:93074997; PMID:1445218
 A:Accession: S29130
 A:Molecule type: mRNA
 A:Residues: 1-384 <TRE>
 A:Cross-references: EMBL:X67598
 A:Accession: T01068
 A>Status: translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-339, 'XTGR', <TFW>
 A:Cross-references: EMBL:X67598; NID:964610; PIDN:CAA47867.1; PID:964611
 A:Experimental source: CNS
 C:Superfamily: calreticulin
 C:Keywords: glycoprotein
 F:381-384/Region: endoplasmic reticulum retention signal

Query Match 85.0%; Score 281; DB 1; Length 405;
 Best Local Similarity 85.0%; Pred. No. 15e-25;
 Matches 51; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 GPGTKVHVIFNYKGNVLINKDIRCKDDFTHTLYTLVRPNTYEVKIDNSQVSGSLE 60
 |||||

Db 134 GPGTKVHVIFNYKGNVLINKDIRCKDDFTHTLYTLVRPNTYEVKIDNSQVSGSLE 193
 |||||

F:316/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 87.4%; Score 278; DB 2; Length 384;
 Best Local Similarity 88.3%; Pred. No. 3.2e-25;
 Matches 53; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 GPGTKVHVIFNYKGNVLINKDIRCKDDFTHTLYTLVRPNTYEVKIDNSQVSGSLE 60
 |||||

Db 110 GPGTKVHVIFNYKGNVLINKDIRCKDDFTHTLYTLVRPNTYEVKIDNSQVSGSLE 169
 |||||

RESULT 9

S29129
 calreticulin precursor (clone 3) - African clawed frog (fragment)
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
 C:Accession: S29129
 R:Traves, S.; Zorzato, F.; Pozzan, T.
 Biochem. J. 287, 579-581, 1992
 A:Title: Identification of calreticulin isoforms in the central nervous system.
 A:Reference number: S29129; PMID:93074997; PMID:1445218
 A:Accession: S29129
 A:Molecule type: mRNA
 A:Residues: 1-411 <TRE>
 A:Cross-references: EMBL:X67597; NID:964608; PIDN:CAA47866.1; PID:964609
 C:Superfamily: calreticulin
 C:Keywords: glycoprotein
 F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
 F:13-411/Product: calreticulin #status predicted <MAT>
 F:408-411/Region: endoplasmic reticulum retention signal
 F:339/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 87.4%; Score 278; DB 2; Length 411;
 Best Local Similarity 88.3%; Pred. No. 3.4e-25;
 Matches 53; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 GPGTKVHVIFNYKGNVLINKDIRCKDDFTHTLYTLVRPNTYEVKIDNSQVSGSLE 60
 |||||

Db 133 GPGTKVHVIFNYKGNVLINKDIRCKDDFTHTLYTLVRPNTYEVKIDNSQVSGSLE 192
 |||||

F:316/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 87.4%; Score 278; DB 2; Length 411;
 Best Local Similarity 88.3%; Pred. No. 3.4e-25;
 Matches 53; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 GPGTKVHVIFNYKGNVLINKDIRCKDDFTHTLYTLVRPNTYEVKIDNSQVSGSLE 60
 |||||

Db 133 GPGTKVHVIFNYKGNVLINKDIRCKDDFTHTLYTLVRPNTYEVKIDNSQVSGSLE 192
 |||||

RESULT 10

A56637
 calreticulin homolog precursor - fruit fly (Drosophila melanogaster)
 N:Alternate names: Ro/SS-A autoantigen/calreticulin homolog
 C:Species: Drosophila melanogaster
 C>Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 13-Aug-1999
 C:Accession: A56637; A37158
 R:Smith, M.J.
 DNA Seq. 3, 247-250, 1992
 A:Title: Nucleotide sequence of a Drosophila melanogaster gene encoding a calreticulin h
 A:Reference number: A56637; PMID:93208374; PMID:1296819
 A:Accession: A56637
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-406 <SMI>
 A:Cross-references: GB:X64461; NID:97685; PIDN:CAA45791.1; PID:97686
 A>Note: sequence extracted from NCBI backbone (NCBIN:128274, NCBI:P:128275)
 R:McCaulliffe, D.P.; Zappi, E.; Lieu, T.S.; Michalak, M.; Sontheimer, R.D.; Capra, J.D.
 J. Clin. Invest. 86, 332-335, 1990
 A:Title: A human Ro/SS-A autoantigen is the homolog of calreticulin and is highly homo

Query Match 87.4%; Score 278; DB 2; Length 411;
 Best Local Similarity 88.3%; Pred. No. 3.4e-25;
 Matches 53; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 GPGTKVHVIFNYKGNVLINKDIRCKDDFTHTLYTLVRPNTYEVKIDNSQVSGSLE 60
 |||||

Db 133 GPGTKVHVIFNYKGNVLINKDIRCKDDFTHTLYTLVRPNTYEVKIDNSQVSGSLE 192
 |||||

F:316/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 87.4%; Score 278; DB 2; Length 411;
 Best Local Similarity 88.3%; Pred. No. 3.4e-25;
 Matches 53; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 GPGTKVHVIFNYKGNVLINKDIRCKDDFTHTLYTLVRPNTYEVKIDNSQVSGSLE 60
 |||||

Db 133 GPGTKVHVIFNYKGNVLINKDIRCKDDFTHTLYTLVRPNTYEVKIDNSQVSGSLE 192
 |||||

F:316/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 87.4%; Score 278; DB 2; Length 411;
 Best Local Similarity 88.3%; Pred. No. 3.4e-25;
 Matches 53; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 GPGTKVHVIFNYKGNVLINKDIRCKDDFTHTLYTLVRPNTYEVKIDNSQVSGSLE 60
 |||||

Db 133 GPGTKVHVIFNYKGNVLINKDIRCKDDFTHTLYTLVRPNTYEVKIDNSQVSGSLE 192
 |||||

F:403-406/Region: endoplasmic reticulum retention signal

Query Match 84.6%; Score 269; DB 2; Length 406;
Best Local Similarity 83.3%; Pred. No. 3.9e-24;
Matches 50; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 GPGTKKVVHVFYNYKGNVINKIRCKDDETHLYTLVIRPDNTYEVKIDNSQVSGSLE 60
|||||
DB 138 GPGTKKVVHVFYNYKGNVINKIRCKDDETHLYTLVIRPDNTYEVKIDNSQVSGSLE 197
|||||

RESULT 11

S71343
calreticulin precursor - Korean frog
C:Species: Rana rugosa (Korean frog)
C:Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 20-Jun-2000
C:Accession: S71343
R:Yamamoto, S.; Nakamura, M.
FEBS Lett. 387, 27-32, 1996
A:Title: Calnexin: its molecular cloning and expression in the liver of the frog, Rana
A:Reference number: S71342; MUID:96234004; PMID:8654561
A:Accession: S71343
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-419 <YAM>
A:Cross-references: EMBL:D78589; NID:gl514956; PIDN:BAAL1425.1; PID:gl514957
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-419/Product: calreticulin #status predicted <MAT>
F:205-213/Region: nuclear location signal
F:415-418/Region: endoplasmic reticulum retention signal

Query Match 82.4%; Score 262; DB 2; Length 419;
Best Local Similarity 83.3%; Pred. No. 2.8e-23;
Matches 50; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 GPGTKKVVHVFYNYKGNVINKIRCKDDETHLYTLVIRPDNTYEVKIDNSQVSGSLE 60
|||||
DB 139 GPGTKKVVHVFYNYKGNVINKIRCKDDETHLYTLVIRPDNTYEVKIDNSQVSGSLE 198
|||||

RESULT 12

A32507
41K larval antigen - nematode (Onchocerca volvulus) (fragment)
C:Species: Onchocerca volvulus
C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 12-Apr-1995
C:Accession: A32507; A28813
R:Unasch, T.R.; Gallin, M.Y.; Soboslay, P.T.; Ertmann, K.D.; Greene, B.M.
J. Clin. Invest. 82, 262-269, 1988
A:Title: Isolation and characterization of expression cDNA clones encoding antigens of
A:Reference number: A92769; MUID:88273584; PMID:2455736
A:Accession: A32507
A:Molecule type: mRNA
A:Residues: 1-336 <UNN>
C:Superfamily: calreticulin

Query Match 76.1%; Score 242; DB 2; Length 336;
Best Local Similarity 75.0%; Pred. No. 5.1e-21;
Matches 45; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 GPGTKKVVHVFYNYKGNVINKIRCKDDETHLYTLVIRPDNTYEVKIDNSQVSGSLE 60
|||||
DB 84 GPGTKKVVHVFYNYKGNVINKIRCKDDETHLYTLVIRPDNTYEVKIDNSQVSGSLE 143
|||||

RESULT 13

A48573
calreticulin autoantigen homolog precursor - fluke (Schistosoma mansoni)
C:Species: Schistosoma mansoni
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A48573
R:Khailaie, J.; Proteine, F.; Schacht, A.M.; Godin, C.; Pierce, R.J.; Capron, A.

Mol. Biochem. Parasitol. 57, 193-202, 1993
A:Title: Cloning of the gene encoding a Schistosoma mansoni antigen homologous to human
A:Reference number: A48573; MUID:93185070; PMID:8433712
A:Accession: A48573
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-393 <KHA>
A:Cross-references: GB:M53097; NID:gl60928
A>Note: sequence inconsistent with the nucleotide translation
A>Note: sequence extracted from NCBI backbone (NCBI:125085, NCBI:125086)
C:Superfamily: calreticulin
F:1-16/Domain: signal sequence #status predicted <SIG>
F:390-393/Region: endoplasmic reticulum retention signal

Query Match 71.4%; Score 227; DB 1; Length 393;
Best Local Similarity 73.3%; Pred. No. 3.6e-19;
Matches 44; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 GPGTKKVVHVFYNYKGNVINKIRCKDDETHLYTLVIRPDNTYEVKIDNSQVSGSLE 60
|||||
DB 136 GPGTKKVVHVFYNYKGNVINKIRCKDDETHLYTLVIRPDNTYEVKIDNSQVSGSLE 195
|||||

RESULT 14

S25851
calreticulin precursor - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 06-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C:Accession: S25851; T33996
R:Smith, M.J.
DNA Seq. 2, 235-240, 1992
A:Title: A. C. elegans gene encodes a protein homologous to mammalian calreticulin.
A:Reference number: S25851; MUID:92329978; PMID:1627827
A:Accession: S25851
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-395 <SMI>
A:Cross-references: EMBL:X59589; NID:g6693; PIDN:CAA42159.1; PID:g6694
R:Bauer, C.; Courtney, L.; Laplant, Y.
submitted to the EMBL Data Library, February 1999
A:Description: The sequence of C. elegans cosmid Y38A10A.
A:Reference number: Z21453
A:Accession: T33996
A>Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-395 <BAU>
A:Cross-references: EMBL:AF125963; PIDN:AAD14746.1; GSPDB:GN00023; CESP:Y38A10A.5
A:Experimental source: strain Bristol N2; clone Y38A10A
C:Genetics:
A:Gene: CESP:Y38A10A.5
A:Map position: 5
A:Introns: 107/3; 315/3
C:Superfamily: calreticulin
F:1-15/Domain: signal sequence #status predicted <SIG>
F:392-395/Region: endoplasmic reticulum retention signal

Query Match 66.2%; Score 210.5; DB 2; Length 395;
Best Local Similarity 66.7%; Pred. No. 3.3e-17;
Matches 40; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

QY 1 GPGTKKVVHVFYNYKGNVINKIRCKDDETHLYTLVIRPDNTYEVKIDNSQVSGSLE 60
|||||
DB 134 GP-TRRVHVLNYKGNVINKIRCKDDETHLYTLVIRPDNTYEVKIDNSQVSGSLE 192
|||||

RESULT 15

T14554
calreticulin - beet
C:Species: Beta vulgaris (beet)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000
C:Accession: T14554
R:Viereck, R.
submitted to the EMBL Data Library, October 1997

A:Description: Nucleotide sequence from sugar beet calreticulin.

A:Reference number: Z18137

A:Accession: T14534

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-416 <VIE>

A:Cross-references: EMBL:AJ002057

A:Experimental source: strain diploide Inzuchtlinie KWS; leaf

C:Superfamily: calreticulin

C:Keywords: calcium binding

Query Match 57.9%; Score 184; DB 2; Length 416;
Best Local Similarity 55.9%; Pred. No. 4.9e-14;
Matches 33; Conservative 9; Mismatches 17; Indels 0; Gaps 0;
QY 1 GPGTKVHVIFNKGKVLINKDIRCKDDEFTLYTLIVRPDNTYEVKIDNSQVESGSL 59
DB 144 GYSTKKVHAIFNNDTNHLIKKDVPCETDQTHVTFILRPDATYSILIDNOEKQTGSL 202

Search completed: October 4, 2004, 13:06:35
Job time : 13.0588 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2004, 12:52:12 ; Search time 8.82353 Seconds
(without alignments)
354.077 Million cell updates/sec

Title: US-09-807-148-8

Perfect score: 318

Sequence: 1 GPQTKKHVIFNYKGNVLI.....PDNTVEVKIDNSQVSGSL 60

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	318	100.0	416	1	CRTC MOUSE
2	318	100.0	416	1	CRTC RAT
3	318	100.0	417	1	CRTC CRIGR
4	318	100.0	417	1	CRTC HUMAN
5	318	100.0	418	1	CRTC RABIT
6	313	98.4	417	1	CRTL BOVIN
7	313	98.4	421	1	CRTC BOVIN
8	269	84.6	406	1	CRTC DROME
9	242	76.1	388	1	RALI ONCVO
10	227	71.4	393	1	CRTC SCHWA
11	210.5	66.2	395	1	CRTC CAEEL
12	199	62.6	420	1	CRTC CHLRE
13	184	57.9	416	1	CRTC BETVU
14	179	56.3	421	1	CRTC PRUAR
15	177.5	55.8	424	1	CRTC DICDI
16	177	55.7	415	1	CRTC RICCO
17	177	55.7	424	1	CRTC ARATH
18	175	55.0	384	1	CRTC HUMAN
19	173	54.4	380	1	CRTC MOUSE
20	172	54.1	425	1	CRTL ARATH
21	171	53.8	424	1	CRTC ORYSA
22	170	53.5	420	1	CRTC MAIZE
23	169	53.1	416	1	CRTC NICPL
24	166	52.2	401	1	CRTC EUGER
25	166	52.2	424	1	CRTC ARATH
26	154	48.4	416	1	CRTC BERST
27	117	36.8	592	1	CALX HUMAN
28	116	36.5	591	1	CALX MOUSE
29	116	36.5	591	1	CALX RAT
30	115	36.2	593	1	CALX CANFA
31	107	33.6	610	1	CALG HUMAN
32	106	33.3	611	1	CALG MOUSE
33	98	30.8	619	1	CALX CAEEL

34	97.5	30.7	560	1	CALX SCHPO
35	87	27.4	546	1	CALX SOYBN
36	82	25.8	530	1	CAX1 ARATH
37	77	24.2	540	1	CALX HELTU
38	77	24.2	551	1	CALX PEA
39	72	22.6	532	1	CAX2 ARATH
40	64.5	20.3	540	1	XTA1 ACICA
41	61.5	19.3	582	1	SYN2 HUMAN
42	61	19.2	474	1	LAM3 MOUSE
43	61	19.2	592	1	LAM2 MOUSE
44	60.5	19.0	586	1	SYN2 RAT
45	59.5	18.7	220	1	PSD9 YEAST

ALIGNMENTS

RESULT 1					
CRTC MOUSE					
ID	CRTC_MOUSE	STANDARD	PRT	416 AA	
AC	P14211;				
DT	01-JAN-1990 (Rel. 13, Created)				
DT	01-JAN-1990 (Rel. 13, Last sequence update)				
DT	15-MAR-2004 (Rel. 43, Last annotation update)				
DE	Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).				
GN	CALR.				
OS	Mus musculus (Mouse).				P36501 schizosacch
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				Q39817 glycine max
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				P29402 arabidopsis
OX	NCBI_TaxID=10090;				Q39994 helianthus
RN	[1]				O82709 pisum sativ
RP	SEQUENCE FROM N.A. AND SEQUENCE OF 18-48 AND 129-161.				Q38798 arabidopsis
RC	STRAIN-BALB/C; TISSUE=Liver;				P25201 acinetobact
RX	MEDLINE=90059555; PubMed=2583110;				Q32777 homo sapien
RA	Smith M.J., Koch G.L.E.;				P48680 mus musculu
RT	"Multiple zones in the sequence of calreticulin (CRP55, calregulin,				P21619 mus musculu
RT	HACBP), a major calcium binding ER/SR protein.";				Q63537 rattus norv
RL	EMBO J. 8:3581-3586(1989).				P40555 saccharomyc
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	MEDLINE=93013037; PubMed=1398135;				
RA	Mazzarella R.A., Gold P., Cunningham M., Green M.;				
RT	"Determination of the sequence of an expressible cDNA clone encoding				
RT	BRP60/calregulin by the use of a novel nested set method.";				
RL	Gene 120:217-225(1992).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRALN=FVB/N-3; TISSUE=Mammary gland;				
RC	MEDLINE=22388257; PubMed=12477932;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,				
RA	Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Wang J., Wang J., Hong F.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,				
RA	Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh T.E.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Udels T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,				
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,				
RA	Schneerch A., Schein J.E., Jones S.J.M., Marra M.A.;				
RT	"Generation and initial analysis of more than 15,000 full-length				
RT	human and mouse cDNA sequences";				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
RN	[4]				
RP	SEQUENCE OF 18-38.				
RC	TISSUE=Fibroblast;				
RX	MEDLINE=95009907; PubMed=7523108;				

RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 using preparative two-dimensional gel electrophoresis.";
 RL Electrophoresis 15:735-745(1994).
 CC -!- FUNCTION: This protein binds calcium. There are both high and
 CC low affinity calcium-binding sites.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -!- SIMILARITY: Belongs to the calreticulin family.
 CC
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EMBL; X14326; CAA33053.1; -;
 DR EMBL; M52988; AAA37569.1; -;
 DR EMBL; BC003453; AA03453.1; -;
 DR PIR; S06763; S06763.
 DR SWISS-2DPAGE; P14211; MOUSE.
 DR MGD; MGI:8252; Calr.
 DR GO; GO:0005509; F:calcium ion binding; IDA.
 DR InterPro; IPR009033; Calreticalex_P.
 DR InterPro; IPR001580; Calreticulin_P.
 DR InterPro; IPR009885; ConA-like_rec_gl.
 DR Pfam; PF00262; calreticulin; 1.
 DR PIRSF; PIRSF002356; Calreticulin; 1.
 DR PRINTS; P00626; CALRETICULIN.
 DR ProDom; PD01866; Calreticulin; 1.
 DR PROSITE; PS00014; ER TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 416 CALRETICULIN.
 FT DOMAIN 18 197 N-DOMAIN.
 FT DOMAIN 198 308 P-DOMAIN.
 FT DOMAIN 309 416 C-DOMAIN.
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
 FT REPEAT 191 202 1-1.
 FT REPEAT 202 221 1-2.
 FT REPEAT 221 238 1-3.
 FT REPEAT 238 255 1-4.
 FT REPEAT 244 255 3 X APPROXIMATE REPEATS.
 FT DOMAIN 259 297 2-1.
 FT REPEAT 259 269 2-2.
 FT REPEAT 273 283 2-3.
 FT REPEAT 287 297 2-3.
 FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
 FT DISULFID 137 163 BY SIMILARITY.
 FT SITE 413 416 PREVENT SECRETION FROM ER.
 SQ SEQUENCE 416 AA; 47994 MW; 24C03B00913408D8 CRC64;

Query Match 100.0%; Score 318; DB 1; Length 416;
 Best Local Similarity 100.0%; Pred. No. 1.le-31;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKHVINYKGNVLINKIRCKDDFTHTLYLIVRPDNTYEVKIDNSQVSGSLE 60
 Db 138 GPGTKKHVINYKGNVLINKIRCKDDFTHTLYLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 2

CRTC_RAT STANDARD; PRT; 416 AA.
 ID CRTC_RAT
 AC P18418; P10452;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60) (CALBP)
 DE (Calcium-binding protein 3) (CABP3).
 GN CALR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain cortex;
 RX MEDLINE=90370496; PubMed=2395661;
 RA Murthy K.K., Banville D., Srikant C.B., Carrier F., Bell A.,
 RA Holmes C., Patel Y.C.;
 RT "Structural homology between the rat calreticulin gene product and
 RT the Onchocerca volvulus antigen Ral-1.";
 RL Nucleic Acids Res. 18:4933-4933(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=93202172; PubMed=8453984;
 RA Nakamura M., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai K.,
 RA Okinaga S., Kobayashi T.;
 RT "An endoplasmic reticulum protein, calreticulin, is transported into
 RT the acrosome of rat sperm.";
 RL Exp. Cell Res. 205:101-110(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=95181573; PubMed=7876339;
 RA Soennichsen B., Fuelektrug J., van Nguyen P., Diekmann W.,
 RA Robinson D.G., Mieskes G.;
 RT "Retention and retrieval: both mechanisms cooperate to maintain
 RT calreticulin in the endoplasmic reticulum.";
 RL J. Cell Sci. 107:2705-2717(1994).
 RN [4]
 RP SEQUENCE OF 270-358 FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX Lone Y.C., Bailly A., Latruffe N.;
 RA Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 18-29.
 RX MEDLINE=91054414; PubMed=2241926;
 RA Traves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
 RA MacLennan D.H., Meldolesi J., Pozzan T.;
 RT "Calreticulin is a candidate for a calsequestrin-like function in
 RT Ca2(+)-storage compartments (calciosomes) of liver and brain.";
 RL Biochem. J. 271:473-480(1990).
 RN [6]
 RP SEQUENCE OF 18-32.
 RC STRAIN=Sprague-Dawley; TISSUE=Testis;
 RX MEDLINE=92360010; PubMed=1497655;
 RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;
 RT "Calreticulin is present in the acrosome of spermatids of rat
 RT testis.";
 RL Biochem. Biophys. Res. Commun. 186:668-673(1992).
 RN [7]
 RP SEQUENCE OF 18-32.
 RC STRAIN=LSC; TISSUE=Liver;
 RX MEDLINE=94072621; PubMed=8251535;
 RA Yokoi T., Nagayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,
 RA Kamataki T.;
 RT "Identification of protein disulfide isomerase and calreticulin as
 RT autoantigenic antigens in LSC strain of rats.";
 RL Biochim. Biophys. Acta 1158:339-344(1993).
 CC -!- FUNCTION: This protein binds calcium. There are both high and low
 CC affinity calcium-binding sites.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -!- SIMILARITY: Belongs to the calreticulin family.
 CC -!- CAUTION: Was originally (Ref.2) thought to be D-beta-
 CC hydroxybutyrate dehydrogenase.
 CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D78308; BAA11345.1; -
CC EMBL; X53363; CAA137446.1; -
CC EMBL; X133702; CAA31987.1; ALT_SEQ.
CC EMBL; X79327; CAA55890.1; -
CC FIR; JH0819; JH0819.
CC PDB; 1HHN; 26-FEB-02.
CC PDB; 1K91; 12-OCT-02.
CC PDB; 1K9C; 12-OCT-02.
CC InterPro; IPR009033; Calret calnex P.
CC InterPro; IPR001580; Calreticulin.
CC InterPro; IPR008985; ConA like lec_gl.
CC InterPro; IPR000886; ER_target_S.
CC Pfam; PF00262; calreticulin; 1.
CC PRINTS; PIRSF002356; Calreticulin; 1.
CC PRODOM; PD001866; Calreticulin; 1.
CC PROSITE; PS00803; CALRETICULIN_1; 1.
CC PROSITE; PS00804; CALRETICULIN_2; 1.
CC PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
CC Endoplasmic reticulum; Calcium-binding; Repeat; Signal; 3D-structure.
CC -----
CC SIGNAL 1 17
CC CHAIN 18 416 CALRETICULIN.
CC FT DOMAIN 18 197 N-DOMAIN.
CC FT DOMAIN 198 308 P-DOMAIN.
CC FT DOMAIN 309 416 C-DOMAIN.
CC FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
CC FT REPEAT 191 202 1-1.
CC FT REPEAT 210 221 1-2.
CC FT REPEAT 227 238 1-3.
CC FT REPEAT 244 255 1-4.
CC FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
CC FT REPEAT 259 269 2-1.
CC FT REPEAT 273 283 2-2.
CC FT REPEAT 287 297 2-3.
CC FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
CC FT DISULFID 137 163 BY SIMILARITY.
CC FT SITE 413 416 PREVENT SECRETION FROM ER.
CC FT SEQUENCE 416 AA; 47995 MW; 2E6713CED31A2970 CRC64;
CC -----
CC Query Match 100.0%; Score 318; DB 1; Length 416;
CC Best Local Similarity 100.0%; Pred. No. 1.1e-31;
CC Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
CC QY 1 GPGTKKHVIFNYKGNVLINKIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 60
CC |
CC DB 138 GPGTKKHVIFNYKGNVLINKIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 197
CC -----
CC RESULT 3
CC CRIC_CRIGR STANDARD; PRT; 417 AA.
CC AC Q8X3H7;
CC DT 28-FEB-2003 (Rel. 41, Created)
CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (Erp60).
CC CALK.
CC GN Cricetus griseus (Chinese hamster).
CC OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
CC OC Cricetus.
CC NCBI_taxID=10029;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RA Chung J.Y.; Lee G.M.;

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: This protein binds calcium. There are both high and low
CC affinity calcium-binding sites.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: Belongs to the calreticulin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AY100688; AAM48568.1; -
CC InterPro; IPR009033; Calret calnex P.
CC InterPro; IPR001580; Calreticulin.
CC InterPro; IPR008985; ConA like lec_gl.
CC InterPro; IPR000886; ER_target_S.
CC Pfam; PF00262; calreticulin; 1.
CC PRINTS; PIRSF002356; Calreticulin; 1.
CC PRODOM; PD001866; Calreticulin; 1.
CC PROSITE; PS00803; CALRETICULIN_1; 1.
CC PROSITE; PS00804; CALRETICULIN_2; 1.
CC PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
CC Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein; Signal.
CC -----
CC SIGNAL 1 17
CC CHAIN 18 417 CALRETICULIN.
CC FT DOMAIN 18 197 N-DOMAIN.
CC FT DOMAIN 198 308 P-DOMAIN.
CC FT DOMAIN 309 417 C-DOMAIN.
CC FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
CC FT REPEAT 191 202 1-1.
CC FT REPEAT 210 221 1-2.
CC FT REPEAT 227 238 1-3.
CC FT REPEAT 244 255 1-4.
CC FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
CC FT REPEAT 259 269 2-1.
CC FT REPEAT 273 283 2-2.
CC FT REPEAT 287 297 2-3.
CC FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
CC FT DISULFID 137 163 BY SIMILARITY.
CC FT SITE 414 417 PREVENT SECRETION FROM ER (POTENTIAL).
CC FT SEQUENCE 417 AA; 48242 MW; D617DA37D14F2D45 CRC64;
CC -----
CC Query Match 100.0%; Score 318; DB 1; Length 417;
CC Best Local Similarity 100.0%; Pred. No. 1.1e-31;
CC Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
CC QY 1 GPGTKKHVIFNYKGNVLINKIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 60
CC |
CC DB 138 GPGTKKHVIFNYKGNVLINKIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 197
CC -----
CC RESULT 4
CC CRIC_HUMAN STANDARD; PRT; 417 AA.
CC AC P27797;
CC DT 01-AUG-1992 (Rel. 23, Created)
CC DT 01-AUG-1992 (Rel. 23, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (Erp60).
CC CALR OR CRPC.
CC GN Homo sapiens (Human).
CC OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CC NCBI_TaxID=9606;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RA MEDLINE=92013129; PubMed=1919005;

RA Rokeach L.A., Haselby J.A., Meilof J.F., Smeenk R.J., Unnasch T.R.,
 RA Greene B.M., Hoch S.O.;
 RA "Characterization of the autoantigen calreticulin.";
 RT J. Immunol. 147:3031-3039(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90237213; PubMed=2332496;
 RA McCaulliffe D.P., Lux F.A., Lieu T.S., Sanz I., Hanke J., Newkirk M.M.,
 RA Bachinski L.L., Itoh Y., Siciliano M.J., Reichlin M., Sontheimer R.D.,
 RA Capra J.D.;
 RT "Molecular cloning, expression, and chromosome 19 localization of a
 RT human Ro/SS-A autoantigen.";
 RT J. Clin. Invest. 85:1379-1391(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92129342; PubMed=1733953;
 RA McCaulliffe D.P., Yang Y.S., Wilson J., Sontheimer R.D., Capra J.D.;
 RT "The 5'-flanking region of the human calreticulin gene shares
 RT homology with the human GRP78, GRP94, and protein disulfide isomerase
 RT promoters.";
 RL J. Biol. Chem. 267:2557-2562(1992).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92129342; PubMed=1733953;
 RA Liu J., Peng X., Yuan J., Qiang B.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92129342; PubMed=1733953;
 RA Lamerdin J.E., McCready P.M., Stilwagen S., Ramirez M., Carrano A.;
 RT "Characterization by genomic sequence analysis of a gene-rich 111 kb
 RT region of 19p13.2 containing the human DNA repair gene, RAD23A.";
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92129342; PubMed=1733953;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosk S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16993(2002).
 RN [7]
 RP SEQUENCE OF 18-36.
 RX MEDLINE=92002034; PubMed=1911778;
 RA Rojiani M.V., Finlay B.B., Gray V., Dedhar S.;
 RT "In vitro interaction of a polypeptide homologous to human Ro/SS-A
 RT antigen (calreticulin) with a highly conserved amino acid sequence in
 RT the cytoplasmic domain of integrin alpha subunits.";
 RL Biochemistry 30:9859-9866(1991).
 RN [8]
 RP SEQUENCE OF 18-32.
 RX MEDLINE=90380058; PubMed=2400400;
 RA Krause K.H., Simmerman H.K.B., Jones L.R., Campbell K.P.;
 RT "Sequence similarity of calreticulin with a Ca2(+)-binding protein
 RT that co-purifies with an Ins(1,4,5)P3-sensitive Ca2+ store in HL-60
 RT cells.";
 RL Biochem. J. 270:545-548(1990).
 RN [9]
 RP SEQUENCE OF 18-28.

RC TISSUE=Liver;
 RX MEDLINE=93162045; PubMed=1286669;
 RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
 RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,
 RA Appel R.D., Hughes G.J.;
 RT "Human liver protein map: a reference database established by
 RT microsequencing and gel comparison.";
 RL Electrophoresis 13:992-1001(1992).
 RN [10]
 RP PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.
 RX TISSUE=Keratinocytes;
 RA MEDLINE=93162043; PubMed=1286667;
 RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Cellis J.E.,
 RA Vandekerckhove J.;
 RT "Microsequences of 145 proteins recorded in the two-dimensional gel
 RT protein database of normal human epidermal keratinocytes.";
 RL Electrophoresis 13:960-969(1992).
 RN [11]
 RP SEQUENCE OF 18-26.
 RX TISSUE=Colon carcinoma;
 RA MEDLINE=97295306; PubMed=9150948;
 RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
 RT "A two-dimensional gel database of human colon carcinoma proteins.";
 RL Electrophoresis 18:605-613(1997).
 CC -1- FUNCTION: This protein binds calcium. There are both high and low
 CC affinity calcium-binding sites.
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: Belongs to the calreticulin family.
 CC -1- CAUTION: Was originally (Ref.2) thought to be the 52 kDa Ro
 CC autoantigen.
 CC
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 CC
 DR EMBL; M84739; AAA51916.1; -;
 DR EMBL; M32294; AAA3582.1; -;
 DR EMBL; AY047586; AAL13126.1; -;
 DR EMBL; AD000092; AAB51176.1; -;
 DR EMBL; BC002500; AAH02500.1; -;
 DR EMBL; BC007911; AAH07911.1; -;
 DR EMBL; BC020493; AAH20493.1; -;
 DR FIR; A42330; A37047.
 DR PDB; 2CUI; 31-MAR-95.
 DR SWISS-2DPAGE; P27797; HUMAN.
 DR Aarhus/Ghent-2DPAGE; 9401; IEF.
 DR HSC-2DPAGE; P27797; HUMAN.
 DR PHCI-2DPAGE; P27797;
 DR PMA-2DPAGE; P27797;
 DR Siena-2DPAGE; P27797;
 DR Genew; HGNC:1455; CALR.
 DR MIM; 109091; -;
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; TAS.
 DR InterPro; IPR009033; Calret calnex P.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR008385; ConA-like leg-gl.
 DR InterPro; IPR000886; ER target_S.
 DR Pfam; PF00262; Calreticulin; 1.
 DR PIRSF; PIRSF002356; Calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR PRODOM; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; 3D-structure.
 FT SIGNAL 1 17
 FT CHAIN 18 417 CALRETICULIN.

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FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 417 C-DOMAIN.
FT REPEAT 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 202 221 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 297 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
FT SITE 137 163 BY SIMILARITY.
FT SITE 414 417 PREVENT SECRETION FROM ER.
FT CONFLICT 35 35 MISSING (IN REF 3).
SQ SEQUENCE 417 AA; 48141 MW; BC37C3C0F1054FB2 CRC64;

Query Match 100.0%; Score 318; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.1e-31;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKHVIFNYKGNVLINKDKDEFTHTLYLVPRDNTYEVKIDNSQVSGSLE 60
DB 138 GPGTKKHVIFNYKGNVLINKDKDEFTHTLYLVPRDNTYEVKIDNSQVSGSLE 197

RESULT 5
CRTC_RABIT
ID -CRTC_RABIT STANDARD; PRT; 418 AA.
AC P15253;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).
GN CALR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Slow-twitch skeletal muscle;
RX MEDLINE=90094320; PubMed=2600080;
RA Flegel L., Burns K., MacLennan D.H., Reithmeier R.A.F., Michalak M.;
RT "Molecular cloning of the high affinity calcium-binding protein
(caltreticulin) of skeletal muscle sarcoplasmic reticulum.";
RL J. Biol. Chem. 264:21522-21528(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fast-twitch skeletal muscle;
RX MEDLINE=91282795; PubMed=2059224;
RA Flegel L., Michalak M.;
RT "Fast-twitch and slow-twitch skeletal muscles express the same
isoform of calreticulin.";
RL Biochem. Biophys. Res. Commun. 177:979-984(1991).
RN [3]
RP SEQUENCE OF 18-36.
RX MEDLINE=91054414; PubMed=2241926;
RA Treves S., de Mattei M., Lanfretti M., Villa A., Green N.M.,
RA MacLennan D.H., Meldolesi J., Pozzan T.;
RT "Calreticulin is a candidate for a calsequestrin-like function in
Ca2(+)-storage compartments (calciosomes) of liver and brain.";
RL Biochem. J. 271:473-480(1990).
RN [4]
RP SEQUENCE OF 18-46.
RX MEDLINE=91201375; PubMed=2016321;
RA Milner R.E., Baksh S., Shemanko C., Carpenter M.R., Smillie L.,
RA Vance J.E., Opas M., Michalak M.;
RT "Calreticulin, and not calsequestrin, is the major calcium binding
protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic
reticulum.";
RL J. Biol. Chem. 266:7155-7165(1991).
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[5]
PP PARTIAL SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=92002038; PubMed=1911780;
RA Guan S., Fallick A.M., Williams D.E., Cashman J.R.;
RT "Evidence for complex formation between rabbit lung flavin-containing
monooxygenase and calreticulin.";
RL Biochemistry 30:9892-9900(1991).
CC -!- FUNCTION: This protein binds calcium. There are both high and low
affinity calcium-binding sites.
CC -!- SUBUNIT: Monomer (by similarity).
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: Belongs to the calreticulin family.
CC
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CC
CC EMBL; J05138; AAA31188.1; -.
DR PIR; A34154; A34154.
DR PIR; C33208; C33208.
DR PIR; S13046; S13046.
DR InterPro; IPR009033; Calret_calnex_P.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR008985; ConA-like lec_gl.
DR InterPro; IPR000886; ER_target_S.
DR Pfam; PF00262; calreticulin_1.
DR PIRSF; PIRSF002356; Calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 418 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 418 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 415 418 PREVENT SECRETION FROM ER.
FT VARIANT 35 35 E -> D.
FT CONFLICT 90 90 P -> T (IN REF. 5).
SQ SEQUENCE 418 AA; 48275 MW; B6082689DC763A6 CRC64;

Query Match 100.0%; Score 318; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 1.1e-31;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKHVIFNYKGNVLINKDKDEFTHTLYLVPRDNTYEVKIDNSQVSGSLE 60
DB 138 GPGTKKHVIFNYKGNVLINKDKDEFTHTLYLVPRDNTYEVKIDNSQVSGSLE 197

RESULT 6
CRTL_BOVIN
ID -CRTL_BOVIN STANDARD; PRT; 417 AA.
AC P52193; Q8SQ53;
```

DT 01-OCT-1996 (Rel. 34, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Calreticulin, brain isoform 1 precursor (CRP55) (Calregulin) (HACBP).
 GN CALR OR CRT.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RC Hossain M.A., Takawa K., Minakata H., Nakajima T.;
 RA "Bovine brain calreticulin";
 RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RN SEQUENCE OF 18-417.
 RP TISSUE=Brain;
 RX MEDLINE=94183174; PubMed=8135753;
 RA Matsuo K., Seta K., Yamakawa Y., Okuyama T., Shinoda T., Isobe T.;
 RT "Covalent structure of bovine brain calreticulin";
 RL Biochem J. 298:435-442(1994).
 CC -!- FUNCTION: This protein binds calcium. There are both high and low
 CC affinity calcium-binding sites.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -!- SIMILARITY: Belongs to the calreticulin family.
 CC
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 CC
 CC EMBL; AB067687; BAB86913.1; -
 DR InterPro; IPR009033; Calret calnex P.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR008985; Cona like lec_gl.
 DR InterPro; IPR000886; ER target_S.
 DR Pfam; PF00262; calreticulin; 1.
 DR PIRSF; PIRSF002356; Calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR PRODOM; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN 1; 1.
 DR PROSITE; PS00804; CALRETICULIN 2; 1.
 DR PROSITE; PS00805; CALRETICULIN REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 417 CALRETICULIN, BRAIN ISOFORM 1.
 FT DOMAIN 18 197 N-DOMAIN.
 FT DOMAIN 198 308 P-DOMAIN.
 FT DOMAIN 309 417 C-DOMAIN.
 FT DOMAIN 151 255 4 X APPROXIMATE REPEATS.
 FT REPEAT 191 202 1-1.
 FT REPEAT 210 221 1-2.
 FT REPEAT 227 238 1-3.
 FT REPEAT 244 255 1-4.
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
 FT REPEAT 259 269 2-1.
 FT REPEAT 273 283 2-2.
 FT REPEAT 287 297 2-3.
 FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
 FT DISULFID 137 163
 FT CARBOHYD 179 179
 FT SITE 414 417 N-LINKED (GLCNAC. . .).
 SQ SEQUENCE 417 AA; 48038 MW; 7BF812C7B5417BE9 CRC64;
 Query Match 98.4%; Score 313; DB 1; Length 417;
 Best Local Similarity 98.3%; Pred. No. 4.4e-31;

Matches 59; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GPGTKKVHVFNYKGNVLINKDCKDEFFHLYTLVIRPNTYEVKIDNSQVSGSLE 60
 Db 138 GPGTKKVHVFNYKGNVLINKDCKDEFFHLYTLVIRPNTYEVKIDNSQVSGSLE 197
 RESULT 7
 CRT2 BOVIN STANDARD; PRT; 421 AA.
 ID -CRT2_BOVIN
 AC P42918;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Calreticulin, brain isoform 2 precursor (CRP55) (Calregulin) (HACBP).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93385184; PubMed=8373827;
 RA Liu N., Fine R.E., Johnson R.J.;
 RT "Comparison of cDNAs from bovine brain coding for two isoforms of
 RT calreticulin";
 RL Biochim. Biophys. Acta 1202:70-76(1993).
 CC -!- FUNCTION: This protein binds calcium. There are both high and low
 CC affinity calcium-binding sites.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -!- SIMILARITY: Belongs to the calreticulin family.
 CC
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 CC
 CC EMBL; L13462; AAC37307.1; -
 DR PIR; S36799; S36799.
 DR InterPro; IPR009033; Calret calnex P.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR008985; Cona like lec_gl.
 DR InterPro; IPR000886; ER target_S-gl.
 DR Pfam; PF00262; calreticulin; 1.
 DR PIRSF; PIRSF002356; Calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR PRODOM; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN 1; 1.
 DR PROSITE; PS00804; CALRETICULIN 2; 1.
 DR PROSITE; PS00805; CALRETICULIN REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 34 POTENTIAL.
 FT CHAIN 35 421 CALRETICULIN, BRAIN ISOFORM 2.
 FT DOMAIN 35 201 N-DOMAIN.
 FT DOMAIN 202 312 P-DOMAIN.
 FT DOMAIN 313 421 C-DOMAIN.
 FT DOMAIN 195 259 4 X APPROXIMATE REPEATS.
 FT REPEAT 195 206 1-1.
 FT REPEAT 214 225 1-2.
 FT REPEAT 231 242 1-3.
 FT REPEAT 248 259 1-4.
 FT DOMAIN 263 301 3 X APPROXIMATE REPEATS.
 FT REPEAT 263 273 2-1.
 FT REPEAT 277 287 2-2.
 FT REPEAT 291 301 2-3.
 FT DOMAIN 366 411 ASP/GLU/LYS-RICH.
 FT DISULFID 141 167 BY SIMILARITY.

RN [1]
RP SEQUENCE FROM N. A.


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CRTC_CABEL STANDARD; PRT; 395 AA.
ID CRTC_CABEL STANDARD; PRT; 395 AA.
AC P27798;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Calreticulin precursor.
GN CCR-1 OR Y38A10A.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoidea; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RC MEDLINE=92329978; PubMed=167827;
RX Smith M.J.;
RA "A. C. elegans gene encodes a protein homologous to mammalian
RT calreticulin.",
RL DNA Seq. 2:235-240 (1992).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RC Bauer C., Courtney L., Laplant Y.;
RA Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
[3]
RN REVISIONS.
RP Waterston R.;
RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL CC -!- FUNCTION: This protein binds calcium. There are both high and low
CC affinity calcium-binding sites.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: Belongs to the calreticulin family.
CC
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CC -----
CC EMBL; X59589; CAA42159.1; -.
CC EMBL; AF125963; AAD14746.1; -.
CC PIR; S25851; S25851.
CC WormPep; Y38A10A.5; CE21562.
CC InterPro; IPR009033; Calret_calmex_P.
CC InterPro; IPR001580; Calreticulin.
CC InterPro; IPR008985; ConA_like Lec-gl.
CC InterPro; IPR000886; ER_target_S.
CC Pfam; PF00262; calreticulin; 1.
CC PIRSF; PIRSF002356; Calreticulin; 1.
CC PRINTS; PR00626; CALRETICULIN.
CC ProDom; PD001866; Calreticulin; 1.
CC PROSITE; PS00014; ER_TARGET; 1.
CC PROSITE; PS00803; CALRETICULIN 1; 1.
CC PROSITE; PS00804; CALRETICULIN 2; 1.
CC PROSITE; PS00805; CALRETICULIN REPEAT; 3.
CC Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
KW SIGNAL
FT SIGNAL 1 15
FT CHAIN 16 395
FT DOMAIN 193 301
FT DOMAIN 302 395
FT DOMAIN 186 250
FT REPEAT 186 197
FT REPEAT 205 216
FT REPEAT 222 233
FT REPEAT 239 250
FT DOMAIN 254 292
FT REPEAT 254 264
FT REPEAT 268 278
FT REPEAT 282 292
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FT DOMAIN 332 390 ASP/GLU/LYS-RICH.
FT DISULFID 133 158 BY SIMILARITY.
FT SITE 392 395 PREVENT SECRETION FROM ER.
SQ SEQUENCE 395 AA; 45616 MW; 35CA7D2EC1D56B03 CRC64;
Query Match 66.2%; Score 210.5; DB 1; Length 395;
Best Local Similarity 66.7%; Pred. No. 1.9e-18;
Matches 40; Conservative 7; Mismatches 12; Indels 1; Gaps 1;
QY 1 GPGTKKHVIFNYKGNVLINKDKCKDEFTHTLTVLRPDNTYEVKIDNSQVESGSL 60
Db 134 GP-TRRVHVLNYKGNKLKKEITCKSDBLTHTLTVLRPDNTYEVKIDNSQVESGSL 192
RESULT 12
CRTC_CHLRE STANDARD; PRT; 420 AA.
ID CRTC_CHLRE STANDARD; PRT; 420 AA.
AC Q9STU3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calreticulin precursor.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=137c / CC-125;
RA Zuppin A., Kaydamov C.;
RT "Cloning and characterization of a cDNA encoding Chlamydomonas
RL reinhardtii calreticulin.",
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: This protein binds calcium. There are both high and low
CC affinity calcium-binding sites (By similarity).
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
CC -!- SIMILARITY: Belongs to the calreticulin family.
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CC -----
CC EMBL; AJ000765; CAB54526.1; -.
CC InterPro; IPR009033; Calret_calmex_P.
CC InterPro; IPR001580; Calreticulin.
CC InterPro; IPR008985; ConA_like Lec-gl.
CC InterPro; IPR000886; ER_target_S.
CC Pfam; PF00262; calreticulin; 1.
CC PIRSF; PIRSF002356; Calreticulin; 1.
CC PRINTS; PR00626; CALRETICULIN.
CC ProDom; PD001866; Calreticulin; 1.
CC PROSITE; PS00014; ER_TARGET; 1.
CC PROSITE; PS00803; CALRETICULIN 1; 1.
CC PROSITE; PS00804; CALRETICULIN 2; 1.
CC PROSITE; PS00805; CALRETICULIN REPEAT; 1.
CC Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
KW SIGNAL
FT SIGNAL 1 18
FT CHAIN 19 420
FT SITE 417 420 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 420 AA; 47327 MW; DD3BAJFF6F61C9B CRC64;
Query Match 62.6%; Score 199; DB 1; Length 420;
Best Local Similarity 61.0%; Pred. No. 5.2e-17;
Matches 36; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
QY 1 GPGTKKHVIFNYKGNVLINKDKCKDEFTHTLTVLRPDNTYEVKIDNSQVESGSL 59
Db 141 GYSTRKHVILTYKGNVLINKDKCKDEFTHTLTVLRPDNTYEVKIDNSQVESGSL 199
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CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: Belongs to the calreticulin family.
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CC -----
CC EMBL; U36937; AAB8719.1; -.
CC DictyBase; DDB001623; ctaA.
CC InterPro; IPR009033; Calret_calnex_P.
CC InterPro; IPR01580; Calreticulin_.
CC InterPro; IPR008985; CnA_like_rec_gl.
CC InterPro; IPR000886; ER_target_S.
CC Pfam; PF00262; calreticulin; 1.
CC PIRSF; PIRSF002356; Calreticulin; 1.
CC PRINTS; PR00626; CALRETICULIN.
CC PRODOM; PD001866; Calreticulin; 1.
CC PROSITE; PS00804; CALRETICULIN_2; 1.
CC PROSITE; PS00805; CALRETICULIN_REPEAT; 1.
CC PROSITE; PS00014; ER_TARGET; 1.
CC Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
KW SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 424 CALRETICULIN.
FT DOMAIN 191 257 4 X 12 AA APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 211 222 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 246 257 1-4.
FT DOMAIN 260 298 3 X 11 AA APPROXIMATE REPEATS.
FT REPEAT 260 270 2-1.
FT REPEAT 274 284 2-2.
FT REPEAT 288 298 2-3.
FT DISULFID 105 137 BY SIMILARITY.
FT SITE 421 424 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 424 AA; 48350 MW; BAF273694FB6FC37 CRC64;
Query Match 55.8%; Score 177.5; DB 1; Length 424;
Best Local Similarity 51.6%; Pred. No. 2.4e-14;
Matches 33; Conservative 14; Mismatches 12; Indels 5; Gaps 2;
Qy 1 GP-----GKKVHVIFNFKGNVLINKDI-RCKDDEFTHLYTLIVRPDNTYEVKIDNSQVE 55
Db 133 GPDVCGASKRVHVILNFKGNHLLKKEINKVETDQLTHQYTLVSPDNTYNVLVDNKEIQ 192
Qy 56 SGSL 59
Db 193 AGNL 196
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Search completed: October 4, 2004, 13:04:02
Job time : 9.82353 secs

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